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Gencore version 4.5

**OM protein - protein search, using sw model**

Run on: March 27, 2002, 15:34:44 ; Search time 15.93 Seconds  
 (without alignments)  
 1898.387 Million cell updates/sec

Title: US-08-774-104A-2

Perfect score: 397

Sequence: 1 MMVYHETRALAGSDLQQLYA.....ENGLKFERPMRQLKDYNHVE 397

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 8

Total number of hits satisfying chosen parameters: 30

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

- 1: PIR:68:\*
- 2: pir2:\*
- 3: pir3:\*
- 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match Length	DB ID	Description
1	10	2.5	511	2 T36306 probable anthranilate synthase component I - Streptomyces coelicolor
2	10	2.5	523	2 A42301 anthranilate synth
3	10	2.5	526	2 T49199 anthranilate synth
4	10	2.5	613	2 T50034 anthranilate synth
5	9	2.3	396	1 A40365 siderophore biosynthetic prote
6	9	2.3	404	2 D86716 anthranilate synth
7	9	2.3	411	2 B64540 anthranilate synth
8	9	2.3	433	2 T43924 anthranilate synth
9	9	2.3	434	2 A75163 anthranilate synth
10	9	2.3	462	2 S03316 anthranilate synth
11	9	2.3	471	1 A65657 probable isochorismate synth
12	9	2.3	485	2 S75655 anthranilate synth
13	9	2.3	494	2 E70352 anthranilate synth
14	9	2.3	494	2 JX0065 anthranilate synth
15	9	2.3	502	2 C83857 anthranilate synth
16	9	2.3	508	2 S19366 anthranilate synth
17	9	2.3	508	2 S75537 anthranilate synth
18	9	2.3	512	2 JH0098 anthranilate synth
19	9	2.3	515	1 NNBSI anthranilate synth
20	9	2.3	621	2 S27752 anthranilate synth
21	9	2.3	621	2 JQ1685 anthranilate synth
22	8	2.0	141	2 E83345 anthranilate synth
23	8	2.0	387	2 E96652 hypothetical protein F23N9.17
24	8	2.0	391	1 SYCII isochorismate synt
25	8	2.0	391	2 D85558 hypothetical protein
26	8	2.0	395	2 A82283 viriohaptin-speci
27	8	2.0	430	2 E64059 probable isochoris
28	8	2.0	441	2 G82612 hypothetical prote
29	8	2.0	474	2 B64434 anthranilate synth

30      8      2.0      616      2      T01990      ALIGNMENTS

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RESULT 1

T36306 probable anthranilate synthase component I - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jan-2000

R:Saunders, D.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, I submitted to the EMBL Data Library, March 1999

A:Reference number: 221604

A:Accession: T36306

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-511 <SAU>

A:Cross-references: EMBL:AL035654; PIDN:CAB38585.1; GSPDB:GN00070; SCORDB:SCE8.07C

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: trpe2; SCORDB:SCE8.07C

C:Superfamily: anthranilate synthase component I

RESULT 2

A42301 Query Match 2.5%; Score 10; DB 2; Length 511; Best Local Similarity 100.0%; Pred. No. 0.082; Mismatches 0; Indels 0; Gaps 0;

C:Accession: A42301

A:Accession: A42301

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-523 <LAM>

A:Title: Genes for tryptophan biosynthesis in the halophilic archaeabacterium Haloferax volcanii

A:Cross-references: GB:M83788; NID:9149036; PIDN:AAA73177.1; PID:9149039

A:Note: the authors failed to give the translation for ACC in residue 239 as shown in C:Superfamily: anthranilate synthase component I

C:Keywords: carbon-carbon lyase; oxo-acid-lyase

Query Match 2.5%; Score 10; DB 2; Length 523; Best Local Similarity 100.0%; Pred. No. 0.084; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY .362 AGAGIVADSD 371

Db 476 AGAGIVADSD 485

RESULT 3

T4199 Query Match 2.5%; Score 10; DB 2; Length 523; Best Local Similarity 100.0%; Pred. No. 0.084; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY .362 AGAGIVADSD 371

Db 483 AGAGIVADSD 492

Submitted to the Protein Sequence Database, April 1 2000

A;Reference number: Z225014  
A;Accession: T49199  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-526 <BEN>  
A;Experimental source: cultivar Columbia; BAC clone F27K19  
A;Gene: ATSP:F27K19.50  
A;Map position: 3  
C;Superfamily: anthranilate synthase component I  
**RESULT 4**  
T50834 Query Match 2.5%; Score 10; DB 2; Length 526;  
C;Species: Ruta graveolens  
C;Best Local Similarity 100.0%; Pred. No. 0.085;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 362 AGAGIVADS 371  
Db 483 AGAGIVADS 492  
R;Pohlmann, J.; DeLuca, V.; Eilett, U.; Martin, W.  
Plant J. 7, 491-501, 1995  
A;Title: Purification and cDNA cloning of anthranilate synthase from Ruta graveolens: mc  
A;Reference number: Z22523; MUID:95276783  
C;Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 02-Sep-2000  
A;Accession: T50834  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-613 <BOH>  
A;Cross-references: EMBL:L34344; PIDN:AAA74901.1  
C;Function: <BAR>  
A;Pathway: tryptophan biosynthesis  
C;Superfamily: biosynthesis of acridone alkaloids  
C;Keywords: carbon-carbon lyase; oxo-acid-lyase  
Query Match 2.5%; Score 10; DB 2; Length 613;  
C;Best Local Similarity 100.0%; Pred. No. 0.097;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 362 AGAGIVADS 371  
Db 572 AGAGIVADS 581  
**RESULT 5**  
A41365 Query Match 2.3%; Score 9; DB 2; Length 396;  
C;Species: Aeromonas hydrophila  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C;Accession: A40365  
R;Barghouthi, S.; Payne, S.M.; Arceneaux, J.E.L.; Byers, B.R.  
J. Bacteriol. 173, 5121-5128, 1991  
A;Title: Cloning, mutagenesis, and nucleotide sequence of a siderophore biosynthetic gene  
A;Reference number: A40365; MUID:91317731  
A;Accession: A40365  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-396 <BAR>  
A;Cross-references: GB:M63319  
A;Note: the authors cloned the codon GAG for residue 393 as GLY  
C;Superfamily: isochorismate synthase  
**RESULT 6**  
D86116 Query Match 2.3%; Score 9; DB 1; Length 396;  
C;Species: Lactococcus lactis subsp. lactis (strain IL140)  
C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 23-Mar-2001  
C;Accession: D86716  
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Eh  
Genome Res. In press, 2001  
A;Title: The complete genome sequence of the lactic acid bacterium.  
A;Reference number: A86625  
A;Accession: D86716  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-404 <STO>  
A;Cross-references: GB:AE00176; NID:912723645; PIDN:AAK04830.1; GSDB:GN00146  
A;Experimental source: strain IL1403; MUID:912723645  
C;Genetics:  
A;Gene: menF  
**RESULT 7**  
B69450 Query Match 2.3%; Score 9; DB 2; Length 404;  
C;Species: Archaeoglobus fulgidus  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 22-Jun-1999  
C;Accession: B69450  
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod  
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E  
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes,  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch  
A;Reference number: A69250; MUID:98049343  
A;Accession: B69450  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-411 <KLE>  
A;Cross-references: GB:AE000992; GB:AE000782; NID:92689315; PIDN:AAB89646.1; PID:9264  
C;Superfamily: anthranilate synthase component I  
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QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 174**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 175**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 176**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 177**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 178**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 179**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 180**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 181**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 182**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 183**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 184**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 185**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 186**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 187**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 188**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 189**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 190**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 191**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 192**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 193**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 194**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 195**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 196**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 197**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 198**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 199**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 200**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 201**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 202**  
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**RESULT 203**  
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**RESULT 204**  
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**RESULT 205**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 206**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 207**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 208**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 209**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 210**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 211**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 212**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 213**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 214**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 215**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 216**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 217**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 218**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 219**  
QY 360 LFAGAGIVVA 368  
Db 358 LFAGAGIVVA 366  
**RESULT 220</b**

C;Species: Pyrococcus kodakaraensis	C;Genetics:
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000	A;Gene: trpE
C;Accession: T43924	C;Superfamily: anthranilate synthase component I
R;Imanaka, T.; Ezaki, S.; Atomi, H.	C;Keywords: carbon-carbon lyase; oxo-acid-lyase
submitted to the EMBL Data Library, July 1999	F;I-462/product: anthranilate synthase component I #status experimental <MAT>
A;Description: Trp operon of Pyrococcus kodakaraensis KOD1.	A;Reference number: Z22725
A;Accession: 42745	A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: DNA	A;Residues: 1-433 <IM>
A;Cross-references: EMBL:AB030011; PIDN:BA82547.1	A;Experimental source: strain KOD1
A;Gene: trpE	C;Genetics:
C;Superfamily: anthranilate synthase component I	C;Gene: trpE
C;Species: anthranilate synthase component I	C;Superfamily: anthranilate synthase component I
C;Accession: 42745	C;Keywords: carbon-carbon lyase; oxo-acid-lyase
QY 362 AGAGIVADS 370	F;I-462/product: anthranilate synthase component I #status experimental <MAT>
Db 401 AGAGIVADS 409	A;Description: Trp operon of Pyrococcus kodakaraensis KOD1.
RESULT 9	A;Reference number: Z22725
A;Best Local Similarity 100.0%; Pred. No. 0.76;	A;Accession: T43924
A;Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	A;Status: preliminary; translated from GB/EMBL/DDJB
C;Species: Pyrococcus abyssi	A;Residues: 1-433 <IM>
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000	A;Experimental source: strain Orsay
C;Accession: A75163	C;Genetics:
R;Anonymous, Genoscope submitted to the EMBL Data Library, July 1999	A;Superfamily: anthranilate synthase component I
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and gene organization	A;Gene: PAB2045
A;Reference number: A75001	A;Cross-references: GB:AJ248284; GB:AL096836; NID:95457730; PIDN:CAB49304.1; PID:9545789
A;Accession: A75163	A;Experimental source: strain Orsay
A;Status: preliminary	C;Genetics:
A;Residues: 1-434 <RAW>	A;Gene: PAB2045
A;Cross-references: GB:AJ248284; GB:AL096836; NID:95457730; PIDN:CAB49304.1; PID:9545789	C;Superfamily: anthranilate synthase component I
Query Match 2.3%; Score 9; DB 2; Length 433;	Query Match 2.3%; Score 9; DB 2; Length 462;
Best Local Similarity 100.0%; Pred. No. 0.76;	Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 362 AGAGIVADS 370	QY 362 AGAGIVADS 370
Db 427 AGAGIVADS 435	Db 427 AGAGIVADS 435
RESULT 11	RESULT 11
A;Accession: A69657	A;Accession: A69657
Probable isochorismate synthase (EC 5.4.99.6) menaquinone-specific menF - Bacillus subtilis	Probable isochorismate synthase (EC 5.4.99.6) menaquinone-specific menF - Bacillus subtilis
C;Species: Bacillus subtilis	C;Species: Bacillus subtilis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000	C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: A69657; S27507; S27508; I13983; T46638; T46639	C;Accession: A69657; S27507; S27508; I13983; T46638; T46639
R;Kunst, F.; Ogasawara, N.; Noszler, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berenbaum, S.; Brondum, S.; Bruschi, C.V.; Caldwell, B.; Capriano, V.; Carter, N.M.; Ehrlich, S.D.; Emmerson, P.T.; Errington, J.; Fabret, C.; Ferrari, Nature 350, 249-256, 1991	R;Kunst, F.; Ogasawara, N.; Noszler, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berenbaum, S.; Brondum, S.; Bruschi, C.V.; Caldwell, B.; Capriano, V.; Carter, N.M.; Ehrlich, S.D.; Emmerson, P.T.; Errington, J.; Fabret, C.; Ferrari, Nature 350, 249-256, 1991
A;Authors: Fouger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Galie, J., Harwood, C.R.; Heaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardon, Y.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parr, V.; Pohl, T.M.; Portetelle, D.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, M.; Sadale, Y.; Scandolo, T.; Scanlan, P.; Sekiguchi, J.; Sekowska, A.; Seakeuchi, M.; Tamashiro, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyai, T.; Winters, P.; Witpat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauri, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parr, V.; Pohl, T.M.; Portetelle, D.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, M.; Sadale, Y.; Scandolo, T.; Scanlan, P.; Sekiguchi, J.; Sekowska, A.; Seakeuchi, M.; Tamashiro, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyai, T.; Winters, P.; Witpat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A.; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis	A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauri, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parr, V.; Pohl, T.M.; Portetelle, D.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, M.; Sadale, Y.; Scandolo, T.; Scanlan, P.; Sekiguchi, J.; Sekowska, A.; Seakeuchi, M.; Tamashiro, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyai, T.; Winters, P.; Witpat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A.; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis
A;Reference number: A69580; MUID:98044033	A;Reference number: A69580; MUID:98044033
A;Accession: A69657	A;Accession: A69657
A;Status: nucleic acid sequence not shown	A;Status: nucleic acid sequence not shown
A;Molecule type: DNA	A;Molecule type: DNA
A;Residues: 1-471 <KUN>	A;Residues: 1-471 <KUN>
A;Cross-references: GB:Z99119; GB:AL009126; NID:92635411; PIDN:CAB15061.1; PID:9263551	A;Cross-references: GB:Z99119; GB:AL009126; NID:92635411; PIDN:CAB15061.1; PID:9263551
A;Experimental source: strain 168	A;Experimental source: strain 168
R;Rowland, B.; Hill, K.; Mueller, J.; Driscoll, J.; Taber, H.	R;Rowland, B.; Hill, K.; Mueller, J.; Driscoll, J.; Taber, H.
submitted to the EMBL Data Library, October 1991	submitted to the EMBL Data Library, October 1991
A;Description: Organization of an operon involved in menaquinone biosynthesis in <i>Bacillus subtilis</i>	A;Description: Organization of an operon involved in menaquinone biosynthesis in <i>Bacillus subtilis</i>
A;Reference number: S27507	A;Reference number: S27507
A;Accession: S27507	A;Accession: S27507
A;Molecule type: DNA	A;Molecule type: DNA
R;Miller, P.	R;Miller, P.
J. Bacteriol. 170: 2742-2748, 1988	J. Bacteriol. 170: 2742-2748, 1988
A;Title: Transcriptional regulation of a promoter in the men gene cluster of <i>Bacillus subtilis</i>	A;Title: Transcriptional regulation of a promoter in the men gene cluster of <i>Bacillus subtilis</i>
A;Accession: I39883	A;Accession: I39883
A;Status: translated from GB/EMBL/DDJB	A;Status: translated from GB/EMBL/DDJB
A;Molecule type: DNA	A;Molecule type: DNA
A;Residues: 1-11, 'K', 13-32 <ML>	A;Residues: 1-11, 'K', 13-32 <ML>
A;Cross-references: GB:M21320; NID:9143178; PIDN:AAA22594.1; PID:9551715	A;Cross-references: GB:M21320; NID:9143178; PIDN:AAA22594.1; PID:9551715
R;Driessens, J.R.; Taber, H.W.	R;Driessens, J.R.; Taber, H.W.
J. Bacteriol. 174: 5063-5071, 1992	J. Bacteriol. 174: 5063-5071, 1992
A;Title: Sequence organization and regulation of the <i>Bacillus subtilis</i> menBE operon.	A;Title: Sequence organization and regulation of the <i>Bacillus subtilis</i> menBE operon.
A;Accession: T46638	A;Accession: T46638
A;Residues: 1-427 <SAT>	A;Residues: 1-427 <SAT>
A;Cross-references: EMBL:X07744; NID:948261; PIDN:CAA30566.1; PID:948263	A;Cross-references: EMBL:X07744; NID:948261; PIDN:CAA30566.1; PID:948263
A;Note: the source is designated as <i>Thermus thermophilus</i> HB8	A;Note: part of this sequence, including the amino end, was confirmed by protein sequenc

A;Cross-references: EMBL:M74521; NID:9557486; PIDN:AAA50396.1; PID:9557487  
A;Accession: T46639  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Cross-references: EMBL:M74521; NID:9557486; PIDN:AAA50397.1; PID:9557488  
A;Genetics:  
A;Gene: menF  
C;Superfamily: isochorismate synthase isomerase  
C;Keywords: intramolecular transferase

Query Match 2.3%; Score 9; DB 1; Length 471;  
Best Local Similarity 100.0%; Pred. No. 0.82;保守性 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12  
S71655 anthranilate synthase (EC 4.1.3.27) component I - Synechocystis sp. (strain PCC 6803)  
N;Intermediate names: protein Sir1979  
C;Species: Synechocystis sp.  
A;Valerie: PCC 6803  
C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000  
C;Accession: S71655  
R;Kanno, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O.; K.; Okumura, S.; Shimpou, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-116, 1996  
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis s.  
A;Reference number: S74322; MUID:97061201  
A;Accession: S75655  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-485 <KANJI>  
A;Cross-references: EMBL:D90912; GB:AB001339; NID:91653228; PIDN:BAA18216.1; PID:9165330  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C;Genetics:  
A;Gene: trpE  
A;Start codon: GTG  
C;Superfamily: anthranilate synthase component I  
C;Keywords: carbon-carbon lyase; oxo-acid-lyase

Query Match 2.3%; Score 9; DB 2; Length 485;  
Best Local Similarity 100.0%; Pred. No. 0.84;保守性 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 363 GAGIVADSD 371  
Db 455 GAGIVADSD 463

RESULT 13  
E70352 anthranilate synthase component I - Aquifex aeolicus  
C;Species: Aquifex aeolicus  
C;Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 22-Jun-1999  
C;Accession: E70352  
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov. Nature 392, 353-358, 1998  
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A;Reference number: A70300; MUID:98196666  
A;Cross-references: GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BAB05378.1; GSDB:G  
A;Accession: E70352  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-494 <KANJI>  
A;Cross-references: GB:AE000596; NID:92983195; PIDN:AC05795.1; PID:92983197; GB:AE00055

Query Match 2.3%; Score 9; DB 2; Length 494;  
Best Local Similarity 100.0%; Pred. No. 0.85;保守性 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 AGAGIVADS 370  
Db 458 AGAGIVADS 466

RESULT 14  
JX0065 anthranilate synthase (EC 4.1.3.27) component I - Clostridium thermocellum  
C;Species: Clostridium thermocellum  
C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 20-Jun-2000  
C;Accession: JX0065  
R;Sato, S.; Nakada, Y.; Hon-nami, K.; Yasui, K.; Shiratsuchi, A.  
J. Biochem. 105, 362-366, 1989  
A;Title: Molecular cloning and the nucleotide sequence of the Clostridium thermocellum A;Reference number: JX0065; MUID:89278056  
A;Accession: JX0065  
A;Molecule type: DNA  
A;Residues: 1-494 <SAT>  
A;Cross-references: GB:D00399; NID:9216420; PIDN:BAA00300.1; PID:9216421  
C;Genetics:  
A;Gene: trpE  
C;Superfamily: anthranilate synthase component I  
C;Keywords: carbon-carbon lyase; oxo-acid-lyase

Query Match 2.3%; Score 9; DB 2; Length 494;  
Best Local Similarity 100.0%; Pred. No. 0.85;保守性 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 AGAGIVADS 370  
Db 459 AGAGIVADS 467

RESULT 15  
C83857 anthranilate synthase trpE [imported] - Bacillus halodurans (strain C-125)  
C;Species: Bacillus halodurans  
C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 08-Dec-2000  
C;Accession: C83857  
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H. Nucleic Acids Res. 28, 4311-4331, 2000  
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a  
A;Reference number: AB3650; MUID:2023314  
A;Accession: C83857  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-502 <STO>  
A;Cross-references: GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BAB05378.1; GSDB:G  
A;Experimental source: strain C-125  
C;Genetics:  
A;Gene: trpE  
C;Superfamily: anthranilate synthase component I

Query Match 2.3%; Score 9; DB 2; Length 502;  
Best Local Similarity 100.0%; Pred. No. 0.86;保守性 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 AGAGIVADS 370  
Db 458 AGAGIVADS 466

Thu Mar 28 13:30:11 2002

us-08-774-104a-2.oli.rpr

Page 5

Search completed: March 27, 2002, 15:40:00  
Job time: 316 sec

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OM protein - protein search, using sw model

Run on: March 27, 2002, 15:39:39 ; Search time 13.3 seconds  
 (Without alignments) 1094.431 Million cell updates/sec

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GenCore version 4.5

Title: US-08-774-104A-2

Perfect score: 397

Sequence: 1 MMTHYHETRALAGSDLQOLYA..... ETLKLKEFPNMRQLKDYNHVE 397

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 10059 seqs, 36664827 residues

Word size : 8

Total number of hits satisfying chosen parameters: 21

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_39;\*

Scored. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Length	DB ID	Description
1	10	2.5	511	1 TRPE_STRCO Q9zaw7 streptomyce
2	10	2.5	523	1 TRPE_HALVO P33975 halobacteri
3	9	2.3	396	1 AMOL_AERHY P23300 aeromonas h
4	9	2.3	411	1 TRPE_ARCFU Q28669 archaeoglob
5	9	2.3	411	1 TRPE_PYRKFQ Q9gb3 pyrococcus
6	9	2.3	462	1 TRPE_THETH P05378 thermus aqu
7	9	2.3	471	1 MENF_BACSU P23973 bacillus su
8	9	2.3	485	1 TRE2_SYN3 P74130 synechocyst
9	9	2.3	494	1 TRPE_AQUAE O66849 aquifex aeo
10	9	2.3	494	1 TRPE_CLOTM P14953 clostridium
11	9	2.3	508	1 TRPE_BACST P30526 bacillus ca
12	9	2.3	508	1 TRPE_BACST Q9x6j4 bacillus st
13	9	2.3	508	1 TRPE_SYN3 P20170 synechocyst
14	9	2.3	513	1 TRPE_BACPU P18257 bacillus pu
15	9	2.3	515	1 TRPE_BACSU P03963 bacillus su
16	9	2.3	621	1 TRPX_ARATH P32069 arabidopsis
17	8	2.0	621	1 ENTC_ECOLI P10377 escherichia
18	8	2.0	395	1 VIBC_VIBCH 007898 vibrio chol
19	8	2.0	403	1 AAT4_ARATH P46646 arabinopolys
20	8	2.0	430	1 MENF_HAETN P46113 haemophilus
21	8	2.0	474	1 TRPE_METJA Q58475 methanococc

**ALIGMENTS**

Result No.	Score	Query Length	DB ID	Description
1	511	AA;	54828 MW;	FA336565GCA4D488 CRC64;
2	523	AA.	523 AA.	
3	523	AA.	523 AA.	
4	362	AA.	371	
5	476	AA.	485	

Query Match Best Local Similarity 2.5%; Score 10; DB 1; Length 511; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db AGAGTVADSD 371

RESULT 2

ID	TRPE_HALVO	STANDARD	PRT;	523 AA.
AC	P33975;			
DT	01-FEB-1994 (Rel. 23, Created)			
DT	01-FEB-1994 (Rel. 23, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	ANTHRANILATE COMPONENT I (EC 4.1.3.27).			
TRPE				
OS	Halobacterium volcanii (Haloflex volvani)			
OC	Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae; Haloflex.			
OX	NCBI_Taxid=2246;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=WELL1;			
RX	MEDLINE=93165748; Pubmed=1537810;			
RA	"Genes for tryptophan biosynthesis in the halophilic archaeabacterium Haloflex volvani: the trpEFG cluster.";			
RT	J. Bacteriol. 174:1694-1697(1992).			
RL				
CC	-I- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE = ANTHRANILATE + PYRUVATE + L-GLUTAMATE.			
CC	-I- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.			
CC	-I- SUBUNIT: TRIMER OF TWO COMPONENTS I AND TWO COMPONENTS II (BY SIMILARITY).			
CC	-I- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES GLUTAMINE AMIDOTRANSFERASE ACTIVITY.			
CC	-I- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I FAMILY.			
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CC	EMBL; AL05654; CAB38585; 1; --;			
DR	InterPro; IPR000350; Chorismate_bind.			
DR	PF00425; chorismate_bind; 1.			
DR	PRINTS; PR00095; ANTSNTASE1.			
DR	ProDom; PF00779; Chorismate_bind; 1.			
KW	Tryptophan biosynthesis; Chorismate; Lyase.			
FRT	DOMAIN 40			
SQ	SEQUENCE 511 AA;			

CC -!- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II (BY  
CC SIMILARITY).

CC -!- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE  
CC USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES  
CC GLUTAMINE AMIDOTRANSFERASE ACTIVITY.

CC -!- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I  
CC FAMILY.

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CC or send an email to license@lsb-sib.ch).

CC

EMBL: M83788; AAAV3177.1; - .

DR PIR: A42301; A42301.

DR InterPro: IPRO00350; chorismate\_bind.

DR Pfam: PF00425; chorismate\_bind; 1.

DR Prodom: PD00779; Chorismate\_bind; 1.

KW Isomerase; Iron transport.

SQ SEQUENCE 395 AA; 42074 MW; 5361F4C18EFAE9D CRC64;

RESULT 4

TRP\_EARCfu STANDARD: PRT: 411 AA.

ID TRP\_EARCfu STANDARD: PRT: 411 AA.

RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;

RX MEDLINE=98049343; PubMed=9389475;

RA Kleink H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,  
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,  
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,  
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,  
Kirnness E.F., Dougherty B.A., McRenney K., Adams M.D., Loftus B.,  
Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,  
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,  
Cotton M.D., Springs T., Artlach P., Kaine B.P., Sykes S.M.,  
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,  
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,  
Ra Venter J.C.;

RA RT "The complete genome sequence of the hyperthermophilic, sulphate-  
reducing archaeon Archaeoglobus fulgidus.";  
RL Nature 390:360-370(1997);

CC -!- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE = ANTHRANILATE +  
RN PYRUVATE + L-GLUTAMATE.

RP SEQUENCE FROM N.A.

RC STRAIN=95A2;

RX MEDLINE=9131731; PubMed=1830579;

RA Bardequin S., Payne S.M., Arceneaux J.E., Byers B.R.,  
RT "Cloning, mutagenesis, and nucleotide sequence of a siderophore  
RT biosynthetic gene (amoa) from Aeromonas hydrophila.;"  
RL Bacteriol. 173:5121-5128(1991).

CC -!- CATALYTIC ACTIVITY: CHORISMATE = ISOCHORISMATE.

CC -!- PATHWAY: AMONABACTIN BIOSYNTHESIS. AMONABACTIN IS AN IRON-  
CHELATING COMPOUND INVOLVED IN TRANSPORTING IRON FROM THE  
CC BACTERIAL ENVIRONMENT INTO THE CELL CYTOPLASM.

CC -!- SIMILARITY: STRONG, TO OTHER ISOCHORISMATE SYNTHASES; WEAK, TO  
CC TRYPTOPHAN AND PABB.

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CC or send an email to license@lsb-sib.ch).

CC

EMBL: M63339; AAA21935.1; - .

DR PIR: A40365; A40365.

DR InterPro: IPRO00350; Chorismate\_bind.

DR Pfam: PF00425; chorismate\_bind; 1.

DR Prodom: PD00779; Chorismate\_bind; 1.

KW Tryptophan biosynthesis; Lyase; Complete proteome.

SQ	SEQUENCE	411 AA:	46346 MW;	2D6591E5BE4A57A CRC64;	AC	P05378;
	Query Match	2.3%	Score 9;	DB 1;	DT	01-NOV-1988 (Rel. 09, created)
	Best Local Similarity	100.0%	Pred. No. 0.31;	Length 411;	DT	01-NOV-1988 (Rel. 09, last sequence update)
	Matches	9;	Conservative	0;	DT	30-MAY-2000 (Rel. 39, last annotation update)
QY	362 AGAGIVADS	370	0;	Mismatches 0;	DE	ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).
DB	381 AGAGIVADS	389	0;	Indels 0;	TRP:	Thermus aquaticus (subsp. thermophilus).
			0;	Gaps 0;	GN	Bacteria; Thermus/Deinococcus group; Thermus group; Thermus.
					OS	NCBI_TAXID=274;
					OC	[1]
					RN	SEQUENCE FROM N.A.
					RP	SEQUENCE FROM N.A.
					RC	STRAIN=HB8 / ATCC 27634;
					RX	MEDLINE=8900781; PubMed=2844259;
					RA	Sato S., Nakada Y., Kanaya S., Tanaka T.;
					RT	"Molecular cloning and nucleotide sequence of Thermus thermophilus HB8 trpE and trpG";
					RL	Biochim. Biophys. Acta 950:303-312(1988).
					CC	-! CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE = ANTHRANILATE + PYRUVATE + L-GLUTAMATE.
					CC	-! PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
					CC	-! SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II (BY SIMILARITY).
					CC	-! MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE USING AMMONIA RATHER THAN GLUTAMINE. WHEREAS COMPONENT II PROVIDES GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
					CC	--
					CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch">http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch</a> ).
					CC	--
					DR	EMBL: X07744; CAA30566_1; -.
					DR	InterPro: IPR000350; chorismate_bind.
					DR	Pfam: PF00425; chorismate_bind; 1.
					DR	PRINTS; PR0095; ANTSNTHASEI.
					DR	Prodrom; PD000779; Chorismate_bind; 1.
					KW	TRYPTOPHAN BIOSYNTHESIS; LYASE.
					SQ	SEQUENCE 462 AA; 51335 MW; 62C9AF94B65B010C CRC64;
					CC	--
					CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch">http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch</a> ).
					CC	--
					DR	EMBL; AB30011; BAA82547_1; -.
					DR	InterPro; IPR000350; chorismate_bind.
					DR	Pfam: PF00425; chorismate_bind; 1.
					DR	PRINTS; PR0095; ANTSNTHASEI.
					DR	Prodrom; PD000779; Chorismate_bind; 1.
					KW	TRYPTOPHAN BIOSYNTHESIS; LYASE.
					SQ	SEQUENCE 433 AA; 48541 MW; E2C539B23365D599 CRC64;
					CC	--
					CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch">http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch</a> ).
					CC	--
					DR	EMBL; AB30011; BAA82547_1; -.
					DR	InterPro; IPR000350; chorismate_bind.
					DR	Pfam: PF00425; chorismate_bind; 1.
					DR	PRINTS; PR0095; ANTSNTHASEI.
					DR	Prodrom; PD000779; Chorismate_bind; 1.
					KW	TRYPTOPHAN BIOSYNTHESIS; LYASE.
					SQ	SEQUENCE 433 AA; 48541 MW; E2C539B23365D599 CRC64;
					CC	--
					DR	EMBL; AB30011; BAA82547_1; -.
					DR	InterPro; IPR000350; chorismate_bind.
					DR	Pfam: PF00425; chorismate_bind; 1.
					DR	PRINTS; PR0095; ANTSNTHASEI.
					DR	Prodrom; PD000779; Chorismate_bind; 1.
					KW	TRYPTOPHAN BIOSYNTHESIS; LYASE.
					SQ	SEQUENCE 433 AA; 48541 MW; E2C539B23365D599 CRC64;
					CC	--
					DR	EMBL; AB30011; BAA82547_1; -.
					DR	InterPro; IPR000350; chorismate_bind.
					DR	Pfam: PF00425; chorismate_bind; 1.
					DR	PRINTS; PR0095; ANTSNTHASEI.
					DR	Prodrom; PD000779; Chorismate_bind; 1.
					KW	TRYPTOPHAN BIOSYNTHESIS; LYASE.
					SQ	SEQUENCE 433 AA; 48541 MW; E2C539B23365D599 CRC64;
					CC	--
					DR	EMBL; AB30011; BAA82547_1; -.
					DR	InterPro; IPR000350; chorismate_bind.
					DR	Pfam: PF00425; chorismate_bind; 1.
					DR	PRINTS; PR0095; ANTSNTHASEI.
					DR	Prodrom; PD000779; Chorismate_bind; 1.
					KW	TRYPTOPHAN BIOSYNTHESIS; LYASE.
					SQ	SEQUENCE 433 AA; 48541 MW; E2C539B23365D599 CRC64;
					CC	--
					DR	EMBL; AB30011; BAA82547_1; -.
					DR	InterPro; IPR000350; chorismate_bind.
					DR	Pfam: PF00425; chorismate_bind; 1.
					DR	PRINTS; PR0095; ANTSNTHASEI.
					DR	Prodrom; PD000779; Chorismate_bind; 1.
					KW	TRYPTOPHAN BIOSYNTHESIS; LYASE.
					SQ	SEQUENCE 433 AA; 48541 MW; E2C539B23365D599 CRC64;
					CC	--
					DR	EMBL; AB30011; BAA82547_1; -.
					DR	InterPro; IPR000350; chorismate_bind.
					DR	Pfam: PF00425; chorismate_bind; 1.
					DR	PRINTS; PR0095; ANTSNTHASEI.
					DR	Prodrom; PD000779; Chorismate_bind; 1.
					KW	TRYPTOPHAN BIOSYNTHESIS; LYASE.
					SQ	SEQUENCE 433 AA; 48541 MW; E2C539B23365D599 CRC64;
					CC	--
					DR	EMBL; AB30011; BAA82547_1; -.
					DR	InterPro; IPR000350; chorismate_bind.
					DR	Pfam: PF00425; chorismate_bind; 1.
					DR	PRINTS; PR0095; ANTSNTHASEI.
					DR	Prodrom; PD000779; Chorismate_bind; 1.
					KW	TRYPTOPHAN BIOSYNTHESIS; LYASE.
					SQ	SEQUENCE 433 AA; 48541 MW; E2C539B23365D599 CRC64;
					CC	--
					DR	EMBL; AB30011; BAA82547_1; -.
					DR	InterPro; IPR000350; chorismate_bind.
					DR	Pfam: PF00425; chorismate_bind; 1.
					DR	PRINTS; PR0095; ANTSNTHASEI.
					DR	Prodrom; PD000779; Chorismate_bind; 1.
					KW	TRYPTOPHAN BIOSYNTHESIS; LYASE.
					SQ	SEQUENCE 433 AA; 48541 MW; E2C539B23365D599 CRC64;
					CC	--
					DR	EMBL; AB30011; BAA82547_1; -.
					DR	InterPro; IPR000350; chorismate_bind.
					DR	Pfam: PF00425; chorismate_bind; 1.
					DR	PRINTS; PR0095; ANTSNTHASEI.
					DR	Prodrom; PD000779; Chorismate_bind; 1.
					KW	TRYPTOPHAN BIOSYNTHESIS; LYASE.
					SQ	SEQUENCE 433 AA; 48541 MW; E2C539B23365D599 CRC64;
					CC	--
					DR	EMBL; AB30011; BAA82547_1; -.
					DR	InterPro; IPR000350; chorismate_bind.
					DR	Pfam: PF00425; chorismate_bind; 1.
					DR	PRINTS; PR0095; ANTSNTHASEI.
					DR	Prodrom; PD000779; Chorismate_bind; 1.
					KW	TRYPTOPHAN BIOSYNTHESIS; LYASE.
					SQ	SEQUENCE 433 AA; 48541 MW; E2C539B23365D599 CRC64;
					CC	--
					DR	EMBL; AB30011; BAA82547_1; -.
					DR	InterPro; IPR000350; chorismate_bind.
					DR	Pfam: PF00425; chorismate_bind; 1.
					DR	PRINTS; PR0095; ANTSNTHASEI.
					DR	Prodrom; PD000779; Chorismate_bind; 1.
					KW	TRYPTOPHAN BIOSYNTHESIS; LYASE.
					SQ	SEQUENCE 433 AA; 48541 MW; E2C539B23365D599 CRC64;
					CC	--
					DR	EMBL; AB30011; BAA82547_1; -.
					DR	InterPro; IPR000350; chorismate_bind.
					DR	Pfam: PF00425; chorismate_bind; 1.
					DR	PRINTS; PR0095; ANTSNTHASEI.
					DR	Prodrom; PD000779; Chorismate_bind; 1.
					KW	TRYPTOPHAN BIOSYNTHESIS; LYASE.
					SQ	SEQUENCE 433 AA; 48541 MW; E2C539B23365D599 CRC64;
					CC	--
					DR	EMBL; AB30011; BAA82547_1; -.
					DR	InterPro; IPR000350; chorismate_bind.
					DR	Pfam: PF00425; chorismate_bind; 1.
					DR	PRINTS; PR0095; ANTSNTHASEI.
					DR	Prodrom; PD000779; Chorismate_bind; 1.
					KW	TRYPTOPHAN BIOSYNTHESIS; LYASE.
					SQ	SEQUENCE 433 AA; 48541 MW; E2C539B23365D599 CRC64;
					CC	--
					DR	EMBL; AB30011; BAA82547_1; -.
					DR	InterPro; IPR000350; chorismate_bind.
					DR	Pfam: PF00425; chorismate_bind; 1.
					DR	PRINTS; PR0095; ANTSNTHASEI.
					DR	Prodrom; PD000779; Chorismate_bind; 1.
					KW	TRYPTOPHAN BIOSYNTHESIS; LYASE.
					SQ	SEQUENCE 433 AA; 48541 MW; E2C539B23365D599 CRC64;
					CC	--
					DR	EMBL; AB30011; BAA82547_1; -.
					DR	InterPro; IPR000350; chorismate_bind.
					DR	Pfam: PF00425; chorismate_bind; 1.
					DR	PRINTS; PR0095; ANTSNTHASEI.
					DR	Prodrom; PD000779; Chorismate_bind; 1.
					KW	TRYPTOPHAN BIOSYNTHESIS; LYASE.
					SQ	SEQUENCE 433 AA; 48541 MW; E2C539B23365D599 CRC64;
					CC	--
					DR	EMBL; AB30011; BAA82547_1; -.
					DR	InterPro; IPR000350; chorismate_bind.
					DR	Pfam: PF00425; chorismate_bind; 1.
					DR	PRINTS; PR0095; ANTSNTHASEI.
					DR	Prodrom; PD000779; Chorismate_bind; 1.
					KW	TRYPTOPHAN BIOSYNTHESIS; LYASE.
					SQ	SEQUENCE 433 AA; 48541 MW; E2C539B23365D599 CRC64;
					CC	--
					DR	EMBL; AB30011; BAA82547_1; -.
					DR	InterPro; IPR000350; chorismate_bind.
					DR	Pfam: PF00425; chorismate_bind; 1.
					DR	PRINTS; PR0095; ANTSNTHASEI.
					DR	Prodrom; PD000779; Chorismate_bind; 1.
					KW	TRYPTOPHAN BIOSYNTHESIS; LYASE.
					SQ	SEQUENCE 433 AA; 48541 MW; E2C539B23365D599 CRC64;
					CC	--
					DR	EMBL; AB30011; BAA82547_1; -.
					DR	InterPro; IPR000350; chorismate_bind.
					DR	Pfam: PF00425; chorismate_bind; 1.
					DR	PRINTS; PR0095; ANTSNTHASEI.
					DR	Prodrom; PD000779; Chorismate_bind; 1.
					KW	TRYPTOPHAN BIOSYNTHESIS; LYASE.
					SQ	SEQUENCE 433 AA; 48541 MW; E2C539B23365D599 CRC64;
					CC	--
					DR	EMBL; AB30011; BAA82547_1; -.
					DR	InterPro; IPR000350; chorismate_bind.
					DR	Pfam: PF00425; chorismate_bind; 1.
					DR	PRINTS; PR0095; ANTSNTHASEI.
					DR	Prodrom; PD000779; Chorismate_bind; 1.
					KW	TRYPTOPHAN BIOSYNTHESIS; LYASE.
					SQ	SEQUENCE 433 AA; 48541 MW; E2C539B23365D599 CRC64;
					CC	--
					DR	EMBL; AB30011; BAA82547_1; -.
					DR	InterPro; IPR000350; chorismate_bind.
					DR	Pfam: PF00425; chorismate_bind; 1.
					DR	PRINTS; PR0095; ANTSNTHASEI.
					DR	Prodrom; PD000779; Chorismate_bind; 1.
					KW	TRYPTOPHAN BIOSYNTHESIS; LYASE.
					SQ	SEQUENCE 433 AA; 48541 MW; E2C539B23365D599 CRC64;
					CC	--
			</td			

RL	Gene 167:105-109(1995).
OC	Bacteria; Cyanobacteria; Chrococccales; Synechocystis;
OX	NCBI_Taxid=1148;
RP	SEQUENCE FROM N.A.
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=98049467; PubMed=9387221;
RA	Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;
"Sequence and functional annotation of the <i>Bacillus subtilis</i> genes in the 200 kb trnB-dnaB region.";	
RT	[3]
RL	Microbiology 143:3431-3441(1997).
RN	PRELIMINARY SEQUENCE FROM N.A.
RC	STRAIN=168 / RBL;
RP	MEDLINE=92332443; PubMed=1629163;
RA	Discoli J.R., Taber H.W.;
RT	"Sequence organization and regulation of the <i>Bacillus subtilis</i> menBE operon.";
RL	J. Bacteriol. 174:5063-5071(1992).
RN	[4]
RP	SEQUENCE OF 1-32 FROM N.A.
RX	MEDLINE=88227858; PubMed=3131310;
RA	Milner P., Mueller J., Hill K., Taber H.W.;
RT	"Transcriptional regulation of a promoter in the men gene cluster of <i>Bacillus subtilis</i> ;"
RL	J. Bacteriol. 170:2742-2748(1988).
CC	-!- CATALYTIC ACTIVITY: CHORISMATE = ISOCHORISMATE.
CC	-!- PATHWAY: MENAQINONE BIOSYNTHESIS.
CC	-!- SIMILARITY: STRONG, TO OTHER ISOCHORISMATE SYNTHASES; WEAK, TO TRPE AND PABB.
CC	-!- CAUTION: USED TO INCLUDE WHAT WAS CALLED 'MENR'.
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CC	-!- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES GLUTAMINE + L-GLUTAMATE.
CC	-!- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
CC	-!- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II (BY SIMILARITY).
CC	DNA Res. 3:1109-1136(1996).
CC	-!- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE = ANTHRANILATE + PYRUVATE + L-GLUTAMATE.
CC	-!- FAMILY: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II (BY SIMILARITY).
CC	-!- CAUTION: THIS IS A DIVERGENT FORM OF TRPE. IT IS NOT OBVIOUS IF IT IS ACTIVE IN TRP BIOSYNTHESIS.
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DR	DR Interpro; IPR000350; Chorismate_bind.
DR	DR Pfam; PF00425; chorismate_bind; 1.
DR	DR PRINTS; PR00095; ANTSNTHASEI.
DR	DR PRODOM; PRO000779; chorismate_bind; 1.
KW	TRYPTOPHAN BIOSYNTHESIS; LYASE; Complete proteome.
SQ	SEQUENCE 485 AA; 54270 MW; 4F2BCCB897BC7C CRC64;
RESULT	8
Query Match	2.3%; Score 9; DB 1; Length 471;
Best Local Similarity	100.0%; Pred. No. 0.35;
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	298 LHPMPALGG 306
Db	376 LHTPALGG 384
RESULT	9
TRPE_AQUAE	
ID	TRPE_AQUAE STANDARD; PRT; 485 AA.
AC	066849;
DT	30-MAY-2000 (Rel. 39, Created)
DT	30-MAY-2000 (Rel. 39, Last sequence update)
DT	20-AUG-2001 (Rel. 40, Last annotation update)
DE	ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).
GN	TRPE OR AQ_582.
OS	Aquifex aeolicus.
OC	Aquifex; Aquificales; Aquificaceae; Aquifex.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=VF5;
RX	MEDLINE=98196666; PubMed=9537220;
RA	Decker G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA	Graham D.E., Overbeek R., Snead M.A., Keller M., Ajayi M., Huber R.,
RA	Feldman R.A., Short J.M., Olson G.J., Stanson R.V.;
RT	"The complete genome of the hyperthermophilic bacterium Aquifex

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 CC  
 DR EMD1;; D00399; BAA00300 1; -. DR PIR; JX0065; JX0065.  
 DR InterPro; IPR00350; Chorismate\_bind.  
 DR PF00425; chorismate\_bind; 1.  
 DR PRINTS; PR00095; ANTSWPHASE1.  
 DR PRODOM; PD00079; Chorismate\_bind; 1.  
 DR TRYPTOPHAN biosynthesis; lyase.  
 SQ SEQUENCE 494 AA; 56020 MW; 32DF1EF2234447D CRC64;

Query	Match	2.3%	Score	9;	DB	1;	Length	494;
QY	Best Local Similarity	100.0%	Pred. No.	0	36;			
Matches	9;	Conservative	Mismatches	0;	Indels	0;	Gaps	0;
Db	459	AGGIVADS	467					

Query Match 2.3%; Score 9; DB 1; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 0.37; Mismatches 0; Indels 0; Gaps 0;

Qy 362 AGAGIVADS 370  
 Db 465 AGAGIVADS 473

**RESULT 12**

TRPE\_BACST TRPE\_BACST STANDARD; PRN: 508 AA.

AC P20170; P20168;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE PROBABLE ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).

GN TRPE OR SLR0738.

OS Synechocystis sp. (strain RCC 6803);  
 OC Bacteria; Chroococcaceae; Synechocystis.  
 OX NCBI\_TaxID=1148;

RN [1]

RP SEQUENCE FROM N.A.

RP STRAIN=TCC 12980 / NCA 26;  
 RX MEDLINE=9929394; PubMed=10369778;

RA Chen X.-P., Antson A.A., Yang M., Baumann C., Dodson E.J.,  
 RA Dodson G.G., Golnick P.;  
 RT "Regulatory features of the trp operon and the crystal structure of  
 the trp RNA-binding attenuation protein from *Bacillus*  
 stearothermophilus.;"  
 RT J. Mol. Biol. 289:1003-1016(1999).  
 CC -I- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE = ANTHRANILATE +  
 PYRUVATE + L-GLUTAMATE.

CC -I- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.

CC -I- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II (BY  
 SIMILARITY).

CC -I- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE  
 USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES  
 GLUTAMINE AMIDOTRANSFERASE ACTIVITY.

CC -I- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I  
 FAMILY.

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CC -----

CC EMBL; AF139534; AAD33791.1; -

DR InterPro; IPR000350; chorismate\_bind.

DR PRINTS; PR00425; chorismate\_bind; 1.

DR PRODOM; PD000779; Chorismate\_bind; 1.

KW tryptophan biosynthesis; Lyase.

SQ SEQUENCE 508 AA; 5640 MW; 25EB252616160ADD CRC64;

Query Match 2.3%; Score 9; DB 1; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 0.37; Mismatches 0; Indels 0; Gaps 0;

Qy 362 AGAGIVADS 370  
 Db 465 AGAGIVADS 473

**RESULT 13**

TRPE\_SYN3 TRPE\_SYN3 STANDARD; PRN: 508 AA.

**RESULT 14**

Query Match 2.3%; Score 9; DB 1; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 0.37; Mismatches 0; Indels 0; Gaps 0;

Qy 363 GAGIVADS 371  
 Db 477 GAGIVADS 485



Thu Mar 28 13:30:11 2002

us-08-774-104a-2.ol.i.rsp

Search completed: March 27, 2002, 15:43:04  
Job time: 205 sec

GenCore version 4.5  
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Q9Pby0 xylella fas  
Q81533 nicotiana t  
Q9be73 macaca fasc

## On protein - protein search, using sw model

Run on:

March 27, 2002, 15:39:09 ; Search time 25.43 Seconds

(without alignments)  
2283.528 Million cell updates/sec

**Title:** US-08-774-104A-2  
**Perfect score:** 397  
**Sequence:** 1 MMVYHETRALAOSDLOOLYA. .... ENGLKEFPMRQLLKDYNHVE 397  
**Scoring table:** OLIGO  
**Gapop:** 60.0 , Gapext 60.0  
**Searched:** 473505 seqs, 146272329 residues  
**Word size :** 8  
**Total number of hits satisfying chosen parameters:** 22  
**Minimum DB seq length:** 0  
**Maximum DB seq length:** 200000000  
**Post-processing:** Listing first 45 summaries

Database : SPTRMBML\_17:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodont:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	339	85.4	398	4 Q9IUA3
2	10	2.5	524	2 Q9490
3	10	2.5	526	1 Q9LY58
4	10	2.5	608	10 Q41155
5	10	2.5	608	10 Q9AW95
6	10	2.5	613	10 Q41156
7	9	2.3	404	2 Q9CHJ9
8	9	2.3	434	1 Q9TIG5
9	9	2.3	453	2 Q99V51
10	9	2.3	502	2 Q9KCB4
11	9	2.3	577	10 Q9XJ30
12	9	2.3	606	10 Q9XJ29
13	8	2.0	55	2 Q9AIP3
14	8	2.0	141	2 Q91166
15	8	2.0	387	10 Q9S169
16	8	2.0	391	2 P95475
17	8	2.0	408	2 Q9f639
18	8	2.0	427	2 Q9e2ZB0
19	8	2.0	436	4 Q9h8r2

## ALIGNMENTS

RESULT	1
Q9IUA3	
ID	Q9IUA3
PRELIMINARY;	
PRM;	398 AA.
AC	Q9IUA3:
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE	NEUTRAL SPHINGOMELINASE.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cattarrhini; Hominidae; Homo.
OX	NCBI_TAXID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE-KIDNEY;
RX	Chatterjee S., Han H., Rollins S., Cleveland T.; Molecular cloning, characterization, and expression of a novel human neutral sphingomyelinase. J. Biol. Chem. 274:37407-37412(1999).
RT	"
RL	EMBL; AF069140; AAF19052.1; -.
DR	InterPro: IPR000550; Chorismate bind.
DR	pfam: PF00425; chorismate_bind; 1.
DR	PRINTS; PRO00095; ANTSWIMASEL.
DR	PRODom: PD000779; Chorismate.bind; 1.
SQ	SEQUENCE 398 AA; 43590 MW; 0248D89974C77BC1 CRC64;
Query Match 85.4% Score 339; DE 4; Length 398;	
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;	
Matches 339; Conservative 0; Neutral 0; Gaps 0;	
QY	59 VFGAQSFEDQEYPOSELMAGNEFWNPENMVTLADKTFGSDATVSDFTTWLAQFVPKOPTN 118
Db	60 VFGAQSFEDQEYPOSELMAGNEFWNPENMVTLADKTFGSDATVSDFTTWLAQFVPKOPTN 119
QY	119 VTFHSHVTDDEVWIERTLENLIDTLAIDQTLAKYVGRQOTLSDTLRQTLAQTLALQAQN 178
Db	120 VTFHSHVTDDEVWIERTLENLIDTLAIDQTLAKYVGRQOTLSDTLRQTLAQTLALQAQN 179
QY	179 TYHWVLRKRHDEFLISATPERLVAMSGQIATAVAGTSRRGFDGADDIALGEALLASQKN 238
Db	180 TYHWVLRKRHDEFLISATPERLVAMSGQIATAVAGTSRRGFDGADDIALGEALLASQKN 239
QY	239 RIEHQYVVAISITRLQVTTSLKVPAMPSLLNKQVQHLYPTGDTAAHLSVTAIVRL 298
Db	240 RIEHQYVVAISITRLQVTTSLKVPAMPSLLNKQVQHLYPTGDTAAHLSVTAIVRL 299
QY	299 HPTPALGGCPVPREALYYTATEKTPRGFLFAGPGYFADNSSEFVGIRSMVNQTORRA 358
Db	300 HPTPALGGCPVPREALYYTATEKTPRGFLFAGPGYFADNSSEFVGIRSMVNQTORRA 359
QY	359 TLEAGACIVADSQAYEETGKLFEPMRQLLKDYNHVE 397
Db	360 TLEAGACIVADSQAYEETGKLFEPMRQLLKDYNHVE 398
RESULT	2
Q9R490	
ID	Q9R490
PRELIMINARY;	
PRM;	524 AA.
AC	Q9R490;
DT	01-JUN-2001 (TREMBLrel. 17, Created)
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE	PARA-AMINOENOATE SYNTHASE, COMPONENT I.

GN	CC2953.							Q41155	ID Q41155 PRELIMINARY; PRT; 608 AA.
OS	Caulobacter crescentus							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
OC	Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
OC	Caulobacter.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
OX	NCBI_TaxID:69394;							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
RN	[1]							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
RP	SEQUENCE FROM N.A.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
RX	Medline+21173698; PubMed=112259647;							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
RA	Nierman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Hatt D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Yamaoka J., Ermolaeva M., White O., Utterback T., Tran K., Wolf A., Vamathevan J., Shetty J., Berry K., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001); TIGR; CC2953; -.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
RA	Embl; AE005959; AAC24915.1; -.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
DR	SEQUENCE 524 AA; 55526 MW; 680D4B427AAAAD5D CRC64;							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
RW	SEQUENCE FROM N.A.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
RX	Ruta graveolens (common rue).							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
RA	Eukaryota; Viriplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; euroids II; Sapindales; Rutaceae; Ruta.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
OC	"Purification and cloning of anthranilate synthase from Ruta graveolens: modes of expression and properties of native and recombinant enzymes.";							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
RT	Ruta graveolens (common rue).							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
RT	Boilmann J., DeLuca V., Eilert U., Martin W.; "Purification and cloning of anthranilate synthase from Ruta graveolens: modes of expression and properties of native and recombinant enzymes.";							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
RT	Ruta graveolens (common rue).							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
RT	Plant J. 7:491-501(1995);							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
RT	EMBL; L33434; AAA74900.1; -.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
DR	HSSP; Q06128; 1QDL.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
DR	Mendel; 12275; Rotgr;433-12275.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
DR	InterPro; IPR000350; Chorismate_bind.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
DR	Pram; PR00425; chorismate_bind; 1.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
DR	PRINTS; PR00095; ANTSNTHASE1.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
DR	PRODOM; PD000779; Chorismate_bind; 1.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
KW	Signal.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
FT	SIGNAL 1 89							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
FT	CHAIN 90 608							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
FT	POTENTIAL.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
FT	ANTHRANILATE SYNTHASE ALPHA SUBUNIT.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
SQ	SEQUENCE 608 AA; 67992 MW; 40F7DB56F49366A5 CRC64;							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
RESULT	3							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
ID	O9LY58							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
ID	O9LY58							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
AC	O9LY58; PRELIMINARY; PRT; 526 AA.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
DT	01-OCT-2000 (TREMBREL. 15, Created)							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
DT	01-OCT-2000 (TREMBREL. 15, Last sequence update)							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
DT	01-JUN-2001 (TREMBREL. 17, Last annotation update)							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
DE	ANTHRANILATE SYNTHASE ALPHA-1 CHAIN-LIKE PROTEIN.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
GN	F27K19.50.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
OS	Arabidopsis thaliana (Mouse-ear cress);							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
OC	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; euroids II; Brassicales; Brassicaceae; Arabidopsis.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
OC	OC							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
NCBI_TaxID:3702;								Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
RN	[1]							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
RP	SEQUENCE FROM N.A.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
RA	Benes V., Wurmback E., Drzeneck H., Ausurge W., Newes H.W., Rudd S., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.; Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
RA	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
RA	[2]							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
RP	SEQUENCE FROM N.A.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
RA	EU Arabidopsis sequencing project;							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
RA	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
DR	EMBL; AL163832; CAB8741.1; -.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
DR	InterPro; IPR000350; Chorismate_bind.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
PRIM:	PF00425; chorismate_bind; 1.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
DR	Prodrom; PD000779; Chorismate_bind; 1.							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
DR	SEQUENCE 526 AA; 59296 MW; AB4D4FD4AA73986C CRC64;							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
RESULT	3							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
Query Match	2.5%; Score 10; DB 10; Length 526;							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
Best Local Similarity	100.0%; Pred. No. 0.26;							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
QY	362 AGAGIVADSD 371							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
Db	483 AGAGIVADSD 492							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
RESULT	4							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
Query Match	2.5%; Score 10; DB 10; Length 608;							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
Best Local Similarity	100.0%; Pred. No. 0.3;							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
QY	362 AGAGIVADSD 371							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.
Db	483 AGAGIVADSD 492							Q41155;	AC Q41155; PRELIMINARY; PRT; 608 AA.

QY	362 AGAGIVADS 371	KW	Complete proteome.
ID		SEQUENCE	404 AA; 46450 MW; 83BFC659F45AB060 CRC64;
AC	Q41156;	PRT;	613 AA.
DT	01-NOV-1996 (TREMBREL. 01, Created)		
DE	01-NOV-1996 (TREMBREL. 01, Last sequence update)		
DT	01-JUN-2001 (TREMBREL. 17, Last annotation update)		
DE	ANTHRANILATE SYNTHASE ALPHA SUBUNIT PRECURSOR.		
OS	Ruta graveolens (common rue).		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE:95276783; PubMed:7757119;		
RA	Bohlmann J., DeLucia V., Elert U., Martin W.;		
RT	"Purification and cDNA cloning of anthranilate synthase from Ruta graveolens: modes of expression and properties of native and recombinant enzymes".		
PL	Plant J. 7:491-501(1995).		
EMBL	U34344; AAH74901.1; -.		
DR	HSSP; Q06128; 1QDL.		
DR	Mendel; 12216; Rutorgr;1433;12276.		
DR	InterPro; IPR000350; Chorismate_bind.		
DR	pfam; PF00425; chorismate_bind; 1.		
DR	PRINTS; PRO0095; ANTSNTHASE1.		
DR	ProDom; PD000779; Chorismate_bind; 1.		
KW	Signal.		
FT	SIGNAL 1 92 POTENTIAL.		
FT	CHAIN 93 613 AA; 67918 MW; 9986339474ABFF75 CRC64;		
SQ	SEQUENCE 613 AA; 67918 MW; 9986339474ABFF75 CRC64;		
Query Match 2.5%; Score 10; DB 10; Length 613; Best Local Similarity 100.0%; Pred. No. 0.3; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	362 AGAGIVADS 371	Query Match 2.3%; Score 9; DB 1; Length 434; Best Local Similarity 100.0%; Pred. No. 2.2; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
DB	572 AGAGIVADS 581	Query Match 2.3%; Score 9; DB 1; Length 434; Best Local Similarity 100.0%; Pred. No. 2.2; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
RESULT 7			
Q9CHJ9	PRELIMINARY; PRT; 404 AA.	RESULT 9	
AC	Q9CHJ9;	ID	099V51
DT	01-JUN-2001 (TREMBREL. 17, Created)	ID	099V51
DT	01-JUN-2001 (TREMBREL. 17, Last sequence update)	AC	Q99V51;
DE	MEMBRANE-SPECIFIC ISOCHORISMATE SYNTHASE (EC 5.4.99.6).	DT	01-JUN-2001 (TREMBREL. 17, Last sequence update)
GN	MEIF.	DT	01-JUN-2001 (TREMBREL. 17, Last sequence update)
OS	Lactococcus lactis (subsp. lactis) (Streptococcus lactis).	DE	SAB095 PROTEIN.
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae; Lactococcus.	GN	
OX	NCBI_TAXID=1360;	OS	
RN	[1]	Staphylococcus aureus subsp. aureus N315.	
RP	SEQUENCE FROM N.A.	OC	Bacteria; Firmicutes; Bacillus/Clostridium group;
RC	STRAIN="IL1403."	OC	Staphylococcus group; Staphylococcus.
RA	Weissenbach J., Ehrlich S.D., Sorokin A.;	OX	NCBI_TAXID=158879;
RA	Boletin A., Wincker P., Mauger S., Jaillon O., Malarme K.,	RN	
RA	"The complete genome sequence of the lactic acid bacterium Lactococcus lactis.", Genome Res. 0:0-0(2001).	RA	Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA	EMBL; AB006306; DAK04330.1; -.	RA	Cui L., Oguchi A., Aoki K.T., Nakai Y., Lian J., Ito T., Kanamori M.,
DR	InterPro; IPR000350; Chorismate_bind.	RA	Matsuura H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Uji Y.,
DR	InterPro; IPR00425; Chorismate_bind; 1.	RA	Takahashi N.K., Sawano T., Inoue R.I., Kaijo C., Sekimizu K.,
DR	ProDom; PD000779; Chorismate_bind; 1.	RA	Hirakawa H., Kubara S., Goto S., Yabuuchi J., Kanematsu M.,
DR	Yamashita A., Oshima K., Furuya C., Yoshino C., Shiba T., Hattori M.,	RA	Ogasawara N., Hayashi H., Hiramatsu K.;

RT	"Whole genome sequencing of meticillin-resistant <i>Staphylococcus aureus</i> ."	RP	SEQUENCE FROM N.A.
RT	Lancet 357:1225-1240(2001).	RC	STRAIN=CV_NIPPONBARE;
RL	Tozawa Y., Hasagawa H., Terakawa T., Wakasa K.;	RA	Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
DR	"Rice cDNA encoding anthranilate synthase alpha subunit."	RT	InterPro; IPR000350; Chorismate_bind; 1.
KW	Complete proteome.	RL	Prints; PR0005; ANTSNTHASET.
SEQUENCE	453 AA; 52245 MW; EOFBD29C30B3161 CRC64;	DR	ProDom; PD000779; Chorismate_bind; 1.
SQ	[1]	DR	HSSP; Q00128; 1QDL.
Query Match	2.3%; Score 9; DB 2; Length 453;	DR	InterPro; IPR000350; Chorismate_bind.
Best Local Similarity	100.0%; Pred. No. 2.3;	PFam	PF00425; chorismate_bind; 1.
Matches	9; Conservative 0; Mismatches 0;	PRINTS	PR0005; ANTSNTHASET.
Indels	0;	DR	ProDom; PD000779; Chorismate_bind; 1.
Gaps	0;	DR	HSSP; Q00128; 1QDL.
Ox	298 LHPPPALGG 306	DR	InterPro; IPR000350; Chorismate_bind.
Db	355 LHPPPALGG 363	DR	Prints; PR0005; ANTSNTHASET.
RESULT	10	DR	ProDom; PD000779; Chorismate_bind; 1.
09KCB4	PRELIMINARY;	DR	HYPOTHETICAL PROTEIN SPY0170.
ID	09KCB4	GN	Streptococcus pyogenes.
AC	09KCB4;	RP	
DT	01-OCT-2000 (TREMBLrel. 15, Created)	RC	
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	STRAIN=CV_NIPPONBARE;	
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)	RA	
DE	ANTHRANILATE SYNTHASE.	RT	
GN	TRPE OR BH1659.	RT	
OS	Bacillus halodurans.	RT	
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;	RT	
OC	Bacillus/Staphylococcus group; Bacillus.	RT	
OX	NCBI_TAXID=86665;	RT	
RN	[1]	RT	
RP	SEQUENCE FROM N.A.	RT	
RC	STRAIN=C-125 / JCM 9153;	RT	
RX	MEDLINE=2051582; PubMed=11058132;	RT	
RA	Takami H., Nakasawa Y., Maeno G., Sasaki R., Masui N.,	RT	
RA	Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuwara S.,	RT	
RA	Horikoshi K.;	RT	
RT	Complete genome sequence of the alkaliophilic bacterium <i>Bacillus halodurans</i> and genomic sequence comparison with <i>Bacillus subtilis</i> ."	RT	
RL	Nucleic Acids Res. 28:317-331(2000).	RT	
EMBL	AB001512; BAB05378.1; -.	RT	
DR	InterPro; IPR000350; Chorismate_bind.	RT	
DR	Pfam; PF00425; chorismate_bind; 1.	RT	
DR	PRINTS; PR0005; ANTSNTHASET.	RT	
DR	ProDom; PD000779; Chorismate_bind; 1.	RT	
KW	Complete proteome.	RT	
SEQUENCE	502 AA; 56349 MN; D844E9AB2689551B CRC64;	RT	
RT	[1]	RT	
RT	halodurans and genomic sequence comparison with <i>Bacillus subtilis</i> .";	RT	
RT	Nucleic Acids Res. 28:317-331(2000).	RT	
EMBL	AB001512; BAB05378.1; -.	RT	
DR	InterPro; IPR000350; Chorismate_bind.	RT	
DR	Pfam; PF00425; chorismate_bind; 1.	RT	
DR	PRINTS; PR0005; ANTSNTHASET.	RT	
DR	ProDom; PD000779; Chorismate_bind; 1.	RT	
KW	Complete proteome.	RT	
SEQUENCE	502 AA; 56349 MN; D844E9AB2689551B CRC64;	RT	
Query Match	2.3%; Score 9; DB 2; Length 502;	RT	
Best Local Similarity	100.0%; Pred. No. 2.6;	RT	
Matches	9; Conservative 0; Mismatches 0;	RT	
Indels	0;	RT	
Gaps	0;	RT	
Ox	362 AGAGIVADS 370	RT	
Db	458 AGAGIVADS 466	RT	
RESULT	11	RT	
09KJ30	PRELIMINARY;	RT	
ID	09KJ30	RT	
AC	09KJ30;	RT	
DT	01-NOV-1999 (TREMBLrel. 12, Created)	RT	
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)	RT	
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)	RT	
DE	ANTHRANILATE SYNTHASE ALPHA 1 SUBUNIT.	RT	
GN	OSASAI.	RT	
OS	Oryza sativa (Rice).	RT	
OC	Eukaryota; Viridiplantae; Streptophytta; Embryophytta; Tracheophytta;	RT	
OC	Spermatophytta; Magnoliophytta; Liliopsida; Poales; Poaceae;	RT	
OC	Embryophytidae; Oryzeae; Oryza.	RT	
OX	NCBI_TAXID=4530;	RT	
RN	[1]	RT	
RP	SEQUENCE FROM N.A.	RT	
RC	STRAIN=CV_NIPPONBARE;	RT	
RA	Tozawa Y., Hasagawa H., Terakawa T., Wakasa K.;	RT	
RT	"Rice cDNA encoding anthranilate synthase alpha subunit."	RT	
RL	Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.	RT	
EMBL	AB002260; BAB02055.1; -.	RT	
DR	HSSP; Q06128; 1QDL.	RT	
DR	InterPro; IPR000350; Chorismate_bind.	RT	
DR	ProDom; IPRO01680; WI40.	RT	
DR	InterPro; IPR000350; Chorismate_bind.	RT	
DR	Pfam; PF00425; chorismate_bind; 1.	RT	
DR	PRINTS; PR0005; ANTSNTHASET.	RT	
DR	ProDom; PD000779; Chorismate_bind; 1.	RT	
PROSITE	PS00678; WD_REPEATS_1; UNKNOWN 1	RT	
SEQUENCE	606 AA; 66988 MW; A74AB7CE98F0608 CRC64;	RT	
Query Match	2.3%; Score 9; DB 10; Length 606;	RT	
Best Local Similarity	100.0%; Pred. No. 3;	RT	
Matches	9; Conservative 0; Mismatches 0;	RT	
Indels	0;	RT	
Gaps	0;	RT	
Ox	362 AGAGIVADS 370	RT	
Db	567 AGAGIVADS 575	RT	
RESULT	13	RT	
09AIP3	PRELIMINARY;	RT	
ID	09AIP3	RT	
AC	09AIP3;	RT	
RT	01-JUN-2001 (TREMBLrel. 17, Created)	RT	
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)	RT	
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)	RT	
DE	HYPOTHETICAL PROTEIN SPY0170.	RT	
GN	Streptococcus pyogenes.	RT	

OC Bacteria; Firmicutes; *Bacillus/Clostridium* group; Streptococcaceae;  
 OC *Saccharococcus*  
 OC NCBI\_TaxID=1314;  
 RN [1] SEQUENCE FROM N. A.  
 RP STRAIN=SF370;  
 RX MEDLINE=21192684; PubMed=11296296;  
 RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,  
 PR Primeaux C., Sezate S., Surovov A.N., Kenton S., Lai H.S., Lin S.P.,  
 RA Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,  
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;  
 RT "Complete genome sequence of an M1 strain of *Saccharococcus pyogenes*."  
 RL PROC. Natl. Acad. Sci. U.S.A. 98:4653-4663(2001).  
 EMBL; AE006486; AAC3270.1; -.  
 KW HYPOTHETICAL PROTEIN; Complete proteome.  
 SQ SEQUENCE 55 AA; 5908 MW; B00EF0F7F137109 CRC64;

Query Match 2.0%; Score 8; DB 2; Length 55;  
 Best Local Similarity 100.0%; Pred. No. 3; 5;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 IATAAVAG 214  
 |||||||  
 DB 10 IATAAVAG 17

RESULT 14  
 ID Q9I166 PRELIMINARY; PRT; 141 AA.  
 AC Q9I166;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DE HYPOTHETICAL PROTEIN PA2415.  
 GN PA2415;  
 OS *Pseudomonas aeruginosa*.  
 OC Bacteria; Proteobacteria; gamma subdivision; pseudomonadaceae;  
 OC *Pseudomonas*.  
 NCBI\_TaxID=287;  
 RN [1]  
 RP SEQUENCE FROM N. A.  
 RC STRAIN=PA01;  
 RX MEDLINE=20437337; PubMed=10984043;  
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,  
 RA Hickey M.J., Brinkman F.S.L., Ruffnagle W.O., Kowalik D.J., Lagrou M.,  
 RA Garber R.L., Goeltz L., Tolentino E., Westbroek-Wadman S., Yuan Y.,  
 RA Brody B.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 RA Reizer J., Sauer M.H., Hancock R.E.W., Lory S., Olson M.V.;  
 RR "Complete genome sequence of *Pseudomonas aeruginosa* PA01, an  
 RR opportunistic pathogen."  
 RL Nature 406:959-964 (2000).  
 DR EMBL; AE004668; AAC05803.1; -.  
 KW HYPOTHETICAL PROTEIN; Complete proteome.  
 SQ SEQUENCE 141 AA; 15171 MW; D6CC5F8B415421E0 CRC64;

Query Match 2.0%; Score 8; DB 2; Length 141;  
 Best Local Similarity 100.0%; Pred. No. 8; 2;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 ALGEALLA 234  
 |||||||  
 DB 125 ALGEALLA 132

RESULT 15  
 Q9SI69 PRELIMINARY; PRT; 387 AA.  
 ID Q9SI69  
 AC Q9SI69;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE F23N19.17.  
 DR Arabidopsis thaliana (mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OC NCBI\_TaxID=3702;  
 RN [1] SEQUENCE FROM N. A.  
 RA Walker M., Shinn P., Brooks S., Buehler E., Chao Q., Dunn P., Khan S.,  
 RA Kim C., Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A.,  
 RA Hansen N.F., Huizar L., Kremenetskaya I., Lenz C., Li J., Liu S.,  
 RA Luoto S., Rovley D., Schwartz J., Toriumi M., Vysotskaya V., Yu G.,  
 RA Davis R.W., Federici N.A., Theologis A., Ecker J.R.;  
 RT "Genomic sequence for *Arabidopsis thaliana* BAC F23N19 from chromosome  
 RT I.";  
 RL Submitted (DCC-1999) to the EMBL/GenBank/DBJ databases.  
 CC -! COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 CC -! SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -! MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC  
 CC ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).  
 CC -! SIMILARITY: TO CLASS\_I OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
 CC AMINOTRANSFERASES.  
 DR EMBL; AC00799; AAC0799; AA\_TRANSFER.CLASS\_1; 1.  
 DR HSSP; P00508; 7AA1.  
 DR InterPro; IPR001511; Aminotran1.  
 DR InterPro; IPR000796; Asp\_Aminotransfse.  
 DR Pfam; PF00155; aminotran\_1; 1.  
 DR PRINTS; PR00799; TRANSAMINASE.  
 DR PROSITE; PS00105; AA\_TRANSFER.CLASS\_1; 1.  
 KW Pyridoxal phosphate.  
 SQ SEQUENCE 387 AA; 42723 MW; 5857C262340B9E1B CRC64;

Query Match 2.0%; Score 8; DB 10; Length 387;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 QOLYAALE 23  
 |||||||  
 DB 337 QOLYAALE 344

Search completed: March 27, 2002, 15:42:44  
 Job time: 215 sec

Thu Mar 28 13:30:11 2002

us-08-774-104a-2.oli.rspt

Title: US-08-774-104a-2  
 Perfect score: 397  
 Sequence: 1 MMTHYETRALAQSDLQQLYA..... ETGSIKFEPMRQLLKDYNHVE 397  
 Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0  
 Searched: 522463 seqs, 71073290 residues  
 Word size : 8  
 Total number of hits satisfying chosen parameters: 20  
 Minimum DB seq length: 0  
 Maximum DB seq length: 200000000  
 Post-processing: Listing first 45 summaries

Database : A\_Geneseq.1101:  
 1: /SIDS8/gcadata/geneseq/geneseq/PAI1980.DAT: \*  
 2: /SIDS8/gcadata/geneseq/geneseq/PAI1981.DAT: \*  
 3: /SIDS8/gcadata/geneseq/geneseq/PAI1982.DAT: \*  
 4: /SIDS8/gcadata/geneseq/geneseq/PAI1983.DAT: \*  
 5: /SIDS8/gcadata/geneseq/geneseq/PAI1984.DAT: \*  
 6: /SIDS8/gcadata/geneseq/geneseq/PAI1985.DAT: \*  
 7: /SIDS8/gcadata/geneseq/geneseq/PAI1986.DAT: \*  
 8: /SIDS8/gcadata/geneseq/geneseq/PAI1987.DAT: \*  
 9: /SIDS8/gcadata/geneseq/geneseq/PAI1988.DAT: \*  
 10: /SIDS8/gcadata/geneseq/geneseq/PAI1989.DAT: \*  
 11: /SIDS8/gcadata/geneseq/geneseq/PAI1990.DAT: \*  
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 15: /SIDS8/gcadata/geneseq/geneseq/PAI1994.DAT: \*  
 16: /SIDS8/gcadata/geneseq/geneseq/PAI1995.DAT: \*  
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 19: /SIDS8/gcadata/geneseq/geneseq/PAI1998.DAT: \*  
 20: /SIDS8/gcadata/geneseq/geneseq/PAI1999.DAT: \*  
 21: /SIDS8/gcadata/geneseq/geneseq/PAI2000.DAT: \*  
 22: /SIDS8/gcadata/geneseq/geneseq/PAI2001.DAT: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description	ALIGNMENTS
1	397	100.0	397 19 AAW69162	Human neutral sph	RESULT 1
2	397	100.0	397 21 AAW68635	Amino acid sequenc	ID AAW69162 standard; Protein: 397 AA.
3	9	2.3	92 20 AAV42118	Wheat anthranilate	ID AAW69162;
4	9	2.3	446 20 AAV42113	Corn anthranilate	XX AC AAW69162;
5	9	2.3	577 20 AAW93815	Rice ASA first iso	XX DT 20-OCT-1998 (first entry)
6	9	2.3	577 20 AAW93816	Rice anthranilate	XX DE Human neutral sphingomyelinase.
7	9	2.3	603 20 AAV42112	Corn anthranilate	XX KW Human; neutral sphingomyelinase; N-Smase; diagnosis; Crohn's disease;
8	9	2.3	606 20 AAW93814	Rice anthranilate	XX KW obesity; diabetes; Alzheimer's disease.
9	9	2.3	615 18 AAW76685	Maize C28 allele a	XX OS Homo sapiens.
10	9	2.3	615 18 AAW76686	Maize anthranilate	XX PD 02-JUL-1998.
11	8	2.0	271 20 AAV33698	E. coli entc prote	XX FT Misc-difference 59 /note= "encoded by GTGTGT"
					XX PR WO828445-A1.
					XX PA (UWTO ) UNIV JOHNS HOPKINS.
					XX PI Chatterjee S;
					XX DR WPI: 1998-377673/32.
					DR N-PADB; AAV41196.
					XX PT Human neutral sphingomyelinase - used to, e.g. treat N-Smase associated disorders, e.g. Crohn's disease, obesity, diabetes, and Alzheimer's disease
					XX PS Claim 19: Page 29-30; 47pp; English.
					XX CC The present sequence represents human neutral sphingomyelinase (N-Smase).
					CC A host cell containing a vector comprising a nucleotide sequence encoding N-Smase can be used to produce N-Smase. N-Smase can be used in a method for identifying a compound useful in the diagnosis or treatment of a human neutral sphingomyelinase related disorder. N-Smase, and a nucleotide sequence encoding N-Smase, can be used for modulating N-Smase activity, and for treating a disorder associated with N-Smase. The
					CC CC N-Smase disorders that can be treated with the nucleotide sequence or N-Smase, is an inflammatory disorder, arthritis, osteoarthritis, Crohn's disease, obesity, diabetes, cirrhosis, susceptible tumours, central nervous system disorder, vascular restenosis, arterial occlusion arising from plaque formation, cardiac disease where LV dysfunction occurs, hypercholesterolaemia, cholesterol ester storage disorder, renal failure, HIV infection, depression, schizophrenia, neurodegeneration, and Alzheimer's disease. An antibody against N-Smase can be used to reduce tumour necrosis factor alpha (TNF-alpha) induced apoptosis of mammalian cells.
					SQ Sequence 397 AA;



	FH Key	Location/Qualifiers
	FT Misc-difference	31 /note= "unspecified"
	FT W0949058-A2.	XX
XX	30-SEP-1999.	
PD		
XX	19-MAR-1999; 99WO-US06046.	
PF		
XX	25-MAR-1998; 98US-0079386.	
PR		
XX	(DUPO ) DU PONT DE NEMOURS & CO E I.	
PA		
XX	Voelmer SJ, Falco SC, Broglie RM, Bryan GT, Cahoon RE;	
PI		
XX	Rafalski JA;	
DR		
DR	WPI; 1999-580451/49.	
N-PSDB;	AZZ25115.	
XX	New isolated tryptophan biosynthetic enzyme nucleic acids, used to produce plants with altered tryptophan levels and for developing herbicides or fungicides -	
XX	Claim 21; Page 64; 83pp; English.	
PS		
CC	The present invention describes isolated anthranilate synthase alpha-subunit (ASAS), anthranilate synthase beta-subunit (ASBS), and tryptophan synthase alpha-subunit (TSAS) nucleic acids, and protein encoded by them, obtained from corn, rice, soybean and wheat cDNA libraries. The nucleic acid fragments may be used to create transgenic plants in which the disclosed ASAS, ASBS or TSAS are present at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found. This would have the effect of altering the level of tryptophan in those cells. Manipulation of the levels of some of the ASAS will also results in changes in the response to pathogen attack. Because this pathway is not followed for the production of tryptophan in higher animals, these enzymes are very good candidates for the discovery of herbicides and fungicides. The ASAS, ASBS or TSAS can be used as targets to facilitate design and/or identification of inhibitors of those enzymes that may be useful as herbicides. Nucleic acid fragments can also be used as probes for genetically and physically mapping the genes that they are a part of, and as markers for traits linked to those genes. Such information may be useful in plant breeding in order to develop lines with desired phenotypes. AZZ25109 to AZZ25127 represent specifically claimed nucleic acids from the present invention and AAY42112 to AAY42130 represent the proteins encoded by them.	
XX	Sequence 92 AA;	
Query Match	2.3%; Score 9; DB 20; Length 92;	
Best Local Similarity	100.0%	
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	362 AGAGIVADS 370	
Db	53 agagivads 61	
RESULT	4	
AAY42113		
ID	AAV42113 standard; Protein; 446 AA.	
XX		
AC	AAY42113;	
XX		
DT	13-DEC-1999 (first entry)	
DE	Corn anthranilate synthase alpha subunit portion protein sequence.	
XX		
Antranilate synthase alpha subunit; tryptophan biosynthetic enzyme; chimeric gene; corn; rice; soybean; wheat; tryptophan synthase; anthranilate synthase beta subunit; herbicide; fungicide; phenotype; pathogen attack; identification; transgenic plant; ASAS; ASBS; TSAS; plant breeding.		
KW		
XW	Zea mays.	
OS		
XX		
Query Match	2.3%; Score 9; DB 20; Length 446;	
Best Local Similarity	100.0%	
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	362 AGAGIVADS 370	
Db	408 agagivads 416	
RESULT	5	
AAW93815		
ID	AAW93815 standard; Protein; 577 AA.	
XX		
AC	AAW93815;	
XX		
DT	25-JUN-1999 (first entry)	
DE	Rice ASA first isozyme alpha-subunit protein variant.	
XX		
KW	Anthranilate synthase; alpha-subunit; ASA; rice; isozyme; plant; seed; maize; wheat; tryptophan content; nutritional value.	
XX		

PT	synthase - used for improving tryptophan production and nutritional value of crops, e.g. rice, maize or wheat
XX	W09911800-A1.
PN	
XX	
PD	11-MAR-1999.
XX	
31-AUG-1998;	98WO-JP03883.
XX	
PR	29-AUG-1997; 97JP-0235049.
XX	
PT	(HOKK ) HOKKO CHEM IND CO LTD.
PA	(NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES.
XX	
PI	Hasegawa H, Terakawa T, Tozawa Y, Wakasa K;
XX	
WPI:	1999-228982/19.
DR	N-PSPDB; AAX23754.
XX	
PT	DNA encodes ^a-subunit of first isozyme of rice anthranilate synthase - used for improving tryptophan production and nutritional value of crops, e.g. rice, maize or wheat
PT	Claim 7; Page 145-147; 152pp; Japanese.
PS	
XX	This invention describes a novel rice anthranilate synthase first isozyme alpha-subunit. The encoding DNA can be used to produce transformant plants and seeds, of e.g. rice, maize or wheat, with enhanced tryptophan content and nutritional value of the crops.
CC	
SQ	Sequence 577 AA;
Db	539 agagivads 547
RESULT	7
ID	AY42112
ID	AY42112 standard; Protein; 603 AA.
XX	
AC	AY42112;
XX	
DT	13-DEC-1999 (first entry)
XX	
DE	Corn anthranilate synthase alpha subunit protein sequence.
XX	
KW	Anthranilate synthase alpha subunit; tryptophan biosynthetic enzyme; chimeric gene; corn; rice; sorghum; wheat; tryptophan synthase; anthranilate synthase beta subunit; herbicide; fungicide; phenotype; pathogen attack; identification; transgenic plant; ASAS; ASBS; TSAS; plant breeding.
KW	
OS	zea mays.
XX	
FH	Key
FT	Location/Qualifiers
FT	Misc-difference 15 /note= "unspecified"
FT	Misc-difference 75 /note= "unspecified"
FT	Misc-difference 115 /note= "unspecified"
FT	
XX	
PN	W09949058-A2.
XX	
PD	30-SEP-1999.
XX	
PF	19-MAR-1999; 99WO-US06046.
XX	
PR	26-MAR-1998; 98US-0079386.
XX	
PA	(DUPO ) DU PONT DE NEMOURS & CO E I.
XX	
PI	Vollmer SJ, Falco SC, Broglie RM, Bryan GT, Cahoon RE;
PI	Rafalski JA;
XX	
DR	WPI; 1999-580431/49.
DR	N-PSPDB; AAZ25109.
XX	
PT	New isolated tryptophan biosynthetic enzyme nucleic acids, used to produce plants with altered tryptophan levels and for developing herbicides or fungicides -
PT	Claim 21; Page 55-57; 83pp; English.
PS	
XX	The present invention describes isolated anthranilate synthase alpha-subunit (ASAS), anthranilate synthase beta-subunit (ASBS), and tryptophan synthase alpha-subunit (TSAS) nucleic acids, and protein
CC	
CC	
CC	
PT	DNA encodes ^a-subunit of first isozyme of rice anthranilate

encoded by them, obtained from corn, rice, soybean and wheat cDNA libraries. The nucleic acid fragments may be used to create transgenic plants in which the disclosed ASAs, ASBS or TSAs are present at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found. This would have the effect of altering the level of tryptophan in those cells. Manipulation of the levels of some of the ASAs will also results in changes in the response to pathogen attack. Because this pathway is not followed for the production of tryptophan in higher animals, these enzymes are very good candidates for the discovery of herbicides and fungicides. The ASAs, ASBS or TSAs can be used as targets to facilitate design and/or identification of inhibitors of those enzymes that may be useful as herbicides. Nucleic acid fragments can also be used as probes for genetically and physically mapping the genes that they are a part of, and as markers for traits linked to those genes. Such information may be useful in plant breeding in order to develop lines with desired phenotypes. AAY25109 to AAY25127 represent specifically claimed nucleic acids from the present invention and AAY42112 to AAY42130 represent the proteins encoded by them.

SQ	Sequence	606 AA;
Query Match	2.3%	Score 9; DB 20; Length 606;
Best Local Similarity	100.0%	Pred. No. 2.6;
Matches	9;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	362 AGAGIVADS 370	
Db	567 agagivads 575	
RESULT	9	
ID	AAW26685	
XX	AAW26685 standard; Protein; 615 AA.	
AC	AAW26685;	
XX		
DT		
XX	27-MAR-1998 (first entry)	

Query Match	2.3%	Score 9;	DB 20:	Length 603;	
Best Local Similarity	100.0%	Pred No.	2.6;		
Matches	9;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
RESULT	8				
AAW93814					
ID	AAW93814	standard; Protein;	606 AA.		
XX					
AC	AAW93814;				
XX					
DE	25-JUN-1999	( first entry)			
XX					
DE	Rice anthranilate synthase second isozyme alpha-subunit protein.				
XX					
KW	Anthranilate synthase; alpha-subunit; ASA; rice; isozyme; plant; seed; maize; wheat; tryptophan content; nutritional value.				
KW	Oryza sativa.				
XX					
OS	xx				
OS	zea mays cell line C28.				
OS					
XX					
XX	W09726366-A1.				
XX					
PD	24-JUL-1997.				
XX					
PF	17-JAN-1997;	97WO-US00983.			
XX					
PR	19-JAN-1996;	96US-0604789.			
XX					
PA	(DEKA ) DERALB GENETICS CORP.				
XX					
PI	Anderson PC, Chomet PS, Griffon MC, Kriz AL;				
XX					
DR	WPI; 1997-385350/35.				
DR	N-PSDB; AAT91102.				
XX					
PT	DNA encoding anthranilate synthase resistant to inhibition by tryptophan - and transformed plants, used e.g. to improve tryptophan levels in plants and as marker for cell selection				
PT					
PT	claim 4; Fig 7; 87pp; English.				
PS					
XX					
CC	This protein sequence comprises a maize anthranilate synthase (AS) that is resistant to inhibition by free L-tryptophan or its amino acid analogues. Its amino acid sequence was deduced from a cDNA clone (see AAT91102) obtained from the 5-methyltryptophan-resistant maize cell line C28. Compared with the wild-type AS sequence (see AAW26086), it contains a single amino acid substitution (Lys for Met-377) at a site implicated in tryptophan feedback sensitivity of the enzyme. The C28 allele AS DNA sequence can be used in claimed methods: (i) to impart tolerance of plants to Trp analogues; (ii) to alter, particularly increase, Trp content of plants, either to increase nutritional value or as source of Trp by extraction; (iii) for production of recombinant AS (used for screening to identify agents that bind or inhibit it); and (iv) for selection of transformed cells. Transgenic plants containing AS can be used for production of proteins or other compounds, including in vitro culture of their cells. The trait of resistance to Trp can be introduced to a wide variety of commercial maize lines.				
CC					
CC					
PS	Claim 3; Page 139-141; 152pp; Japanese.				
XX					
PT	DNA encodes a subunit of first isozyme of rice anthranilate synthase - used for improving tryptophan production and nutritional value of crops, e.g. rice, maize or wheat				
PT					
XX	Hasegawa H, Terakawa T, Tozawa Y, Wakasa K;				
XX					
DR	WPI: 1999-22892/19.				
DR	N-PSDB; AATX23753.				
XX					
CC	This invention describes a novel rice anthranilate synthase first isozyme alpha subunit. The encoding DNA can be used to produce transgenic plants and seeds, of e.g. rice, maize or wheat, with enhanced tryptophan content and nutritional value of the crops.				
CC					
CC					
SQ	Sequence 615 AA;				

Query Match 2.3%; Score 9; DB 18; Length 615;  
 Best Local Similarity 100.0%; Pred. No. 2.7;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 362 AGAGIVADS 370  
 Db 576 agagivads 584

|||||||

RESULT 10  
 AAW26685 standard; Protein; 615 AA.  
 XX  
 AC AAY3698;  
 XX  
 DT 27-MAR-1998 (first entry)  
 XX  
 DE Maize anthranilate synthase alpha subunit.  
 XX  
 KW Anthranilate synthase; L-tryptophan; tolerance; resistance;  
 KW transgenic plant; maize; selectable marker.  
 XX  
 OS Zea mays inbred line Va26.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..46 /label= Transit\_peptide  
 XX  
 WO9726366-A1.  
 XX  
 PD 24-JUL-1997.  
 XX  
 PF 17-JAN-1997; 97WO-US00983.  
 XX  
 PR 19-JAN-1996; 96US-0604789.  
 XX  
 PA (DEKA-) DEKALB GENETICS CORP.  
 XX  
 PT Anderson PC, Chomet PS, Griffon MC, Kriz AL;  
 XX  
 DR WPI; 1997-385350/35.  
 XX  
 DR N-PADB; AAT91103.

XX  
 PT DNA encoding anthranilate synthase resistant to inhibition by  
 PT tryptophan and transformed plants, used e.g. to improve tryptophan  
 PT levels in plants and as marker for cell selection  
 XX  
 PS Claim 7; Fig 3; 87pp; English.

XX  
 CC This protein sequence comprises a maize anthranilate synthase (AS)  
 CC alpha subunit encoded by a cDNA clone (see AAT91103) obtained from  
 CC inbred line Va26. It differs at only 1 residue (Met-377 for Lys)  
 CC from the alpha subunit (see AAW26685) of a maize allele C28 AS that  
 CC is resistant to inhibition by free L-tryptophan or its amino acid  
 CC analogues. Maize AS sequences, especially those from the C28  
 CC allele, can be used in claimed methods: (i) to impart tolerance of  
 CC plants to Trp analogues; (ii) to alter, particularly increase, the  
 CC Trp content of plants, either to increase nutritional value or as a  
 CC source of Trp by extraction; (iii) for production of recombinant AS  
 CC (used for screening to identify agents that bind to or inhibit it);  
 CC and (iv) for selection of transformed cells. Transgenic plants  
 CC containing AS can be used for production of proteins or other  
 CC compounds, including in vitro culture of their cells. The trait of  
 CC resistance to Trp can be introduced to a wide variety of commercial  
 CC maize lines.

SQ Sequence 615 AA;

Query Match 2.0%; Score 8; DB 20; Length 271;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 360 LFAGAGIV 367  
 Db 238 lfqagiv 245

|||||||

RESULT 12  
 AAB08519  
 ID AAB08519 standard; Protein; 287 AA.  
 XX  
 AC AAB08519;  
 XX  
 DT 20-DEC-2000 (first entry)  
 XX  
 DE Protein encoded by haemoglobin-response gene HBR2.  
 XX  
 KW Haemoglobin-response gene; HBR1; HBR2; HBR3; haemoglobin; adhesion;  
 disseminated infection; blastoconidia; fibronectin.  
 XX  
 OS Candida albicans.  
 XX  
 PN WO200050601-A2.  
 XX  
 PD 31-AUG-2000.  
 XX  
 PF 18-JAN-2000; 2000WO-US01184.  
 XX  
 PR 26-FEB-1999; 99US-0258634.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PT Robertts DD, Yan S;  
 XX  
 DR WPI; 2000-543913/49.  
 XX  
 PT detecting disseminated Candida albicans infections using  
 hemoglobin-response genes and proteins, probes and antibodies derived  
 from them -  
 XX  
 PS Claim 3; Page 50-51; 54pp; English.  
 XX  
 CC The present sequence is encoded by a haemoglobin-response  
 gene. The expression also describes haemoglobin-response  
 genes HBR1 and HBR3. The expression of these genes is specifically  
 induced when the organism is exposed to haemoglobin during disseminated  
 infections. Haemoglobin induces increased adhesion of C. albicans  
 blastoconidia to fibronectin. HBR1, HBR2 and HBR3 nucleic acid probes,  
 proteins and antibodies are used for the diagnosis of disseminated  
 C. albicans infections.  
 XX  
 SQ Sequence 287 AA;

Query Match 2.0%; Score 8; DB 21; Length 287;  
 Best Local Similarity 100.0%; Pred. No. 13; Mismatches 8; Conservative 0; Indels 0; Gaps 0;  
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GAVATPA 35  
 Db 248 gayfatpa 255

RESULT 13  
 AAM00815  
 ID AAM00815 standard; Protein; 313 AA.  
 XX  
 AC AAM00815;  
 XX  
 DT 01-OCT-2001 (first entry)  
 XX  
 DE Human bone marrow protein, SEQ ID NO: 178.  
 XX  
 KW Human; bone marrow; antiinflammatory; cytostatic; neuroprotective;  
 antiviral; antibacterial; antifungal; anti-HIV; haemostatic;  
 immuno-suppressive; gene therapy; cytokine cell proliferation;  
 cell differentiation modulator; immune disorder; infection; cancer;  
 human immunodeficiency virus; HIV; autoimmune disorder; haemophilia.  
 XX

---

OS Homo sapiens.  
 XX  
 PN WO200153453-A2.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PR 23-DEC-2000; 2000WO-US34960.  
 XX  
 PR 21-JAN-2000; 2000US-0488725.  
 PR 25-APR-2000; 2000US-052317.  
 PR 09-JUL-2000; 2000US-058042.  
 PR 19-JUL-2000; 2000US-060312.  
 PR 03-AUG-2000; 2000US-0653450.  
 PR 14-SEP-2000; 2000US-066191.  
 PR 19-OCT-2000; 2000US-0693036.  
 PR 30-NOV-2000; 2000US-0250583.  
 XX  
 PA (HYSEQ-) HYSEQ INC.  
 XX  
 PI Ford JE, Boyle BJ, Tang YT, Liu C, Asundi V, Chen R, Ma Y;  
 PI Ren F, Wang J, Werbman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 PI Zhao QA, Zhou P, Drmanac R;  
 XX  
 DR WPI; 2001-488707/3.  
 DR N-PSDB; AHH8934.

XX  
 PT Novel bone-marrow-expressed polynucleotides and polypeptides, useful  
 for treating e.g. cancer and immune deficiency disorders -  
 XX  
 PS Claim 10; Page 334-335; 648pp; English.  
 XX  
 CC The present sequence is one of 251 novel human polypeptides encoded  
 by a bone marrow-expressed polynucleotide. The polynucleotide and the  
 polypeptide encoded by it are useful in the treatment of various  
 immune deficiencies and disorders. The deficiencies and disorders may  
 be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal  
 infection, or may result from an autoimmune disorder, a coagulation  
 disorder (e.g. haemophilia), inhibition of tumour cell proliferation,  
 suppression of an inflammatory response or treatment of a nervous  
 system disorder such as Alzheimer's disease. Detection of the presence  
 or increased expression of the polynucleotide or the protein it  
 encodes is useful for the diagnosis and/or prognosis of one  
 or more types of cancer. The polynucleotide and polypeptide can be  
 used as nutritional sources or supplements and in the screening of  
 chemical compounds as potential drugs.  
 XX  
 SQ Sequence 313 AA;

Query Match 2.0%; Score 8; DB 22; Length 313;  
 Best Local Similarity 100.0%; Pred. No. 14; Mismatches 8; Conservative 0; Indels 0; Gaps 0;  
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 151 VFGROOTL 158  
 Db 157 vfgrqgtl 164

RESULT 14  
 AAY0338  
 ID AAY0338 standard; Protein; 331 AA.  
 XX  
 AC AAY50338;  
 XX  
 DT 14-JAN-2000 (first entry)  
 XX  
 DE P. fluorescens ICS orfA protein fragment.  
 XX  
 KW Isochorismate synthase; ICS; plant; pathogen resistance; chitinase;  
 pathogen inducible promoter; antipathogenic protein; toxin;  
 antifungal protein; albumin-type protein; hypersensitive response.  
 XX  
 OS Pseudomonas fluorescens.

XX WO9950423-A2.

XX 25-MAR-1999; 99WO EP02176.

XX PD 07-OCT-1999.

XX XX

XX PR 25-MAR-1999; 99WO-EP02176.

XX PF 31-MAR-1998; 98US-0080203.

XX PR 03-APR-1998; 98US-0080625.

XX PA (MOGE-) MOGEN INT NV.

XX PA (UYLE-) RIJKSUNIV LEIDEN.

XX PA (UYNI-) UNIV Nijmegen.

XX PR 31-MAR-1998; 98US-0080203.

XX PA (MOGE-) MOGEN INT NV.

XX PA (UYLE-) RIJKSUNIV LEIDEN.

XX PA (UYNI-) UNIV Nijmegen.

XX PT Linthorst HJM, Verpoorte R, Verberne MC, Moreno PRH;

XX PI Van Tegelen LJP, Willems GJ, Croes AF, Stuiver MH, Custers J;

XX PI Simons LH, Melchers LS, Bol JF;

XX DR WPI; 1999-610856/52.

XX DR WPI; 1999-610856/52.

XX DR N-PSDB; A4Z23755.

XX PT Method for inducing pathogen resistance in plants -

XX DR N-PSDB; A4Z23755.

XX PS Example 3; Page 51-53; 66pp; English.

XX CC This invention describes a novel method for the induction of pathogen resistance in plants, by transformation with an expression cassette harboring a gene coding for an isochorismate synthase (ICS). A pathogen inducible promoter can be used to drive expression of a heterologous protein. The heterologous protein used in the method of the invention is an antipathogenic protein e.g. chitinase, glucanase, osmotin, lectins, saccaride oxidase, oxalate oxidase, magainins, toxins from *Bacillus thuringiensis*, or antifungal proteins isolated from *Mirabilis jalapa*, *Amaranthus*, *Raphanus*, *Brassica*, *Sinapis*, *Arabidopsis*, *Dahlia*, *Cnicus*, *Lathyrus*, *Clitoria*, *Allium* seeds, *Aralia* and *Impatiens* and albumin-type proteins, such as trionine, napin, barley trypsin inhibitor, cereal gliadin and wheat-alpha-amylase, or a protein that can induce a hypersensitive response, such as Cf, Bs3 and Po proteins from tomato and N-protein from tobacco. This sequence represents the *Escherichia coli* isochorismate synthase entC gene which is described in the method of the invention.

XX CC

XX SQ Sequence 391 AA;

XX Query Match 2.0%; Score 8; DB 20; Length 391;

XX Best Local Similarity 100.0%; Pred. No. 18;

XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 360 LFAGAGIV 367

Db 358 lfagagiv 365

XX

XX RESULT\_15

XX AAY50335 standard; Protein: 391 AA.

XX ID AAY50335;

XX AC

XX DT 14-JAN-2000 (first entry)

DE E. coli entC protein.

XX Isochorismate synthase; ICS; Plant; pathogen resistance; chitinase; pathogen inducible promoter; antipathogenic protein; toxin; entC; antifungal protein; albumin-type protein; hypersensitive response.

XX OS Escherichia coli.

XX PN WO9950423-A2.

XX PD 07-OCT-1999.

XX

XX Search completed: March 27, 2002, 15:39:37

XX Job time: 293 sec

GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on:

March 27, 2002, 15:34:44 ; Search time 12.6 Seconds

(without alignments)  
709.032 Million cell updates/sec

Title: US-08-774-104A-2

Perfect score: 397

Sequence: 1 MMVYHETRALAQSDLQQLYA.....ENGLKFEDPMRQLLKDYNHVE 397

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 212252 seqs, 22503292 residues

Word size : 8

Total number of hits satisfying chosen parameters: 8

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

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2: /cgn2_6/ptodata/2/iaa5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaaPCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaaBackfiles1.pep:*
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**pred.** No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	397	100.0	397	US-08-774-104A-2
2	9	2.3	604	US-08-604-789B-2
3	9	2.3	604	US-08-604-789B-16
4	9	2.3	604	US-09-312-721A-2
5	9	2.3	604	US-09-312-721A-16
6	9	2.3	621	US-08-604-789B-4
7	9	2.3	621	US-08-312-721A-4
8	8	2.0	616	US-09-001-826-5

## ALIGNMENTS

RESULT 1 US-08-774-104A-2  
; Sequence 2, Application US/08774104A  
; Patent No. 5919687  
; GENERAL INFORMATION:  
; APPLICANT: Chatterjee, Subroto  
; TITLE OF INVENTION: RECOMMENDANT N-SHASES AND NUCLEIC ACIDS  
; TITLE OF INVENTION: ENCODING SAME  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dile, Bronstein, Roberts & Cushman, LLP  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: MA

COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/774,104A  
FILING DATE: 12/24/96  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Corless, Peter F  
REGISTRATION NUMBER: 33,860  
REFERENCE/DOCKET NUMBER: 46906  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 397 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: Linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
US-08-774-104A-2

Query Match Score: 100.0%; Score: 397; DB: 2; Length: 397;  
Best Local Similarity: 100.0%; Pred. No.: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 MMVYHETRALAQSDLQQLYA.....ENGLKFEDPMRQLLKDYNHVE 60  
Db 1 MMVYHETRALAQSDLQQLYALETTERGAYFATPADDTLRFGIGAIATAKTAQALOGAVF 60  
Db 61 GAQSFDCEQYPOSELMAGFWPEVMVTLAIDKITFGSDTVSFTTWLAQFVPKQPNIVT 120  
Db 61 GAQSFDCEQYPOSELMAGFWPEVMVTLAIDKITFGSDTVSFTTWLAQFVPKQPNIVT 120  
QY 121 TSHVTDDEVWIERTENLDTLADQTLLAKVNGRQDQLSDTIRLAQIIRALEQANTY 180  
Db 121 TSHVTDDEVWIERTENLDTLADQTLLAKVNGRQDQLSDTIRLAQIIRALEQANTY 180  
Db 181 HVVLRKRHDLFLSATPERLUVAMSGGQIATAAVAGTSRGTDGADDIALGEALIASQRNRI 240  
Db 181 HVVLRKRHDLFLSATPERLUVAMSGGQIATAAVAGTSRGTDGADDIALGEALIASQRNRI 240  
Db 241 EHQYVVAASITTRLQDVPSLKVAMPMSLKKNKQVQHLYTPITGDIAAHLSVTAIVDRLHP 300  
Db 241 EHQYVVAASITTRLQDVPSLKVAMPMSLKKNKQVQHLYTPITGDIAAHLSVTAIVDRLHP 300  
QY 301 TPALGVVRREALYYIATHEKPRGLFAGPIGFADMSGEFWVGIRSSMMVNQTORRATL 360  
Db 301 TPALGVVRREALYYIATHEKPRGLFAGPIGFADMSGEFWVGIRSSMMVNQTORRATL 360  
QY 361 FAGAGIVADSQOYEETGKLFEPMRQLLKDYNHVE 397  
Db 361 FAGAGIVADSQOYEETGKLFEPMRQLLKDYNHVE 397

RESULT 2 US-08-604-789B-2  
; Sequence 2, Application US/08604789B  
; Patent No. 6118047

GENERAL INFORMATION:

APPLICANT: Anderson, P.C.  
Chomet, P.S.  
Griffor, M.C.

Kriz, A. L.

TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE  
AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN  
OVERPRODUCTION

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.  
STREET: P. O. Box 2938  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/604,789B  
FILING DATE: 19-Jan-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>  
REGISTRATION NUMBER: 30,440  
REFERENCE/DOCKET NUMBER: 950.026US1  
ATTORNEY/AGENT INFORMATION:  
NAME: Woessner, Warren D.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (612) 373-6903  
TELEFAX: (612) 339-3061  
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 604 amino acids

TYPE: amino acid

STRANDEDNESS: single

MOLECULE TYPE: protein

TOPOLogy: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-08-604-789B-2

Query Match 2.3%; Score 9; DB 3; Length 604;  
Best Local Similarity 100.0%; Pred. No. 0.88;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 604 amino acids

TYPE: amino acid

STRANDEDNESS: single

MOLECULE TYPE: protein

TOPOLogy: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-08-604-789B-16

RESULT 4  
US-09-312-721A-2

Query Match 2.3%; Score 9; DB 3; Length 604;  
Best Local Similarity 100.0%; Pred. No. 0.88;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE 2, Application US/09312721A  
PATENT NO. 6271016

GENERAL INFORMATION:

APPLICANT: Anderson, P.C.  
Chomet, P.S.  
Griffor, M.C.

Kriz, A. L.

TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE  
AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN  
OVERPRODUCTION

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.  
STREET: P. O. Box 2938  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/312,721A  
FILING DATE: 17-May-1999

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08,604,789  
FILING DATE: 19-JAN-1996

ATTORNEY/AGENT INFORMATION:

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.  
STREET: P. O. Box 2938  
CITY: Minneapolis  
STATE: MN

NAME: Woessner, Warren D.  
 REGISTRATION NUMBER: 30,440  
 REFERENCE/DOCKET NUMBER: 950, 026US2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (612) 373-6903  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 604 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 MOLECULE DESCRIPTION: SEQ ID NO: 2:  
 US-09-312-721A-2

RESULT 5  
 US-09-312-721A-16  
 ; Sequence 16, Application US/09312721A  
 ; Patent No. 6271016  
 GENERAL INFORMATION:  
 APPLICANT: Anderson, P.C.  
 Chomet, P.S.  
 Griffor, M.C.  
 Kriz, A.L.  
 TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE  
 AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN  
 OVERPRODUCTION  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Schweigman, Lundberg, Woessner & Kluth, P. A.  
 STREET: P.O. Box 2938  
 CITY: Minneapolis  
 STATE: MN  
 COUNTRY: USA  
 ZIP: 55402  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM Compatible  
 MEDIUM TYPE: Diskette  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/604,789B  
 FILING DATE: 19-Jan-1996  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: <Unknown>  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Woessner, Warren D.  
 REGISTRATION NUMBER: 30,440  
 REFERENCE/DOCKET NUMBER: 950, 026US1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (612) 373-6903  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 621 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 MOLECULE DESCRIPTION: SEQ ID NO: 4:  
 US-08-604-789B-4

Query Match 2,3%; Score 9; DB 3; Length 621;  
 Best Local Similarity 100.0%; Pred. No. 0; 0; 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0;  
 Gaps 0;

RESULT 6  
 US-08-604-789B-4  
 ; Sequence 4, Application US/08604789B  
 ; Patent No. 6118047  
 GENERAL INFORMATION:  
 APPLICANT: Anderson, P.C.  
 Chomet, P.S.  
 Griffor, M.C.  
 Kriz, A.L.  
 TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE  
 AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN  
 OVERPRODUCTION  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Schweigman, Lundberg, Woessner & Kluth, P. A.  
 STREET: P.O. Box 2938  
 CITY: Minneapolis  
 STATE: MN  
 COUNTRY: USA  
 ZIP: 55402  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM Compatible  
 MEDIUM TYPE: Diskette  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/604,789B  
 FILING DATE: 19-Jan-1996  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: <Unknown>  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Woessner, Warren D.  
 REGISTRATION NUMBER: 30,440  
 REFERENCE/DOCKET NUMBER: 950, 026US1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (612) 373-6903  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 621 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 MOLECULE DESCRIPTION: SEQ ID NO: 4:  
 US-08-604-789B-4

Query Match 2,3%; Score 9; DB 3; Length 604;  
 Best Local Similarity 100.0%; Pred. No. 0; 0; 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0;  
 Gaps 0;

Qy 362 AGAGIVADS 370  
 Db 565 AGAGIVADS 573

Qy 362 AGAGIVADS 370  
 Db 565 AGAGIVADS 573

RESULT 7

US 09-312-721A-4  
 Sequence 4 Application US/09312721A  
 Patent No. 6271016

GENERAL INFORMATION:  
 APPLICANT: Anderson, P.C.  
 Chomet, P.S.  
 Griffor, M.C.

Kriz, A. L.  
 Kriz, A. L.

TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE  
 AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN  
 OVERPRODUCTION

NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS: Schwengen, Lundberg, Woessner & Kluth, P. A.  
 STREET: P. O. Box 2938  
 CITY: Minneapolis  
 STATE: MN  
 COUNTRY: USA  
 ZIP: 55402

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette:  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/312,721A  
 FILING DATE: 17-May-1999  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/04,789  
 FILING DATE: 19-JAN-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Woessner, Warren D.  
 REGISTRATION NUMBER: 30,440  
 REFERENCE/DOCKET NUMBER: 950.026US2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (612) 373-6903  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 621 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-312-721A-4

Query Match 2.0%; Score 8; DB 2; Length 616;  
 Best Local Similarity 100.0%; Pred. No. 9,4;  
 Matches 8; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy	363	GAGIVADS	370
Db	543	GAGIVADS	550

Search completed: March 27, 2002, 15:39:05  
 Job time: 261 sec

RESULT 8  
 US-09-001-826-5  
 Sequence 5, Application US/09001826A  
 Patient No. 596527  
 GENERAL INFORMATION:  
 APPLICANT: SONG, HEE-SOOK  
 APPLICANT: BROTHERTON, JEFFREY E.  
 APPLICANT: WIDHOLM, JACK M  
 TITLE OF INVENTION: SELECTABLE MARKER AND PROMOTER FOR PLANT TISSUE CULTURE  
 TITLE OF INVENTION: SELECTABLE MARKER AND TRANSFORMATION  
 FILE REFERENCE: U101.C1  
 CURRENT APPLICATION NUMBER: US/09/001,826A  
 CURRENT FILING DATE: 1997-12-31  
 EARLIER APPLICATION NUMBER: 08/937,739; 60/025,140  
 EARLIER FILING DATE: 1997-07-25; 1996-07-26

Thu Mar 28 13:30:10 2002

us-08-774-104a-2.olr.ra

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